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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 15, 2005, 02:48:24 ; Search time 4914 Seconds  
(without alignments)  
2987.776 Million cell updates/sec

Title: US-10-715-665-7\_COPY\_1\_303

Perfect score: 1746

Sequence: 1 MDAMKRGGLCCVLLCGAVFV.....AACNWTGRGCRDLEDRDSE 303

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Database :

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4: gb.cm.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
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11: gb.sts.\*  
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13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1746	100.0	5882	6 AX154501	AX154501 Sequence
2	1620.5	92.8	1207	6 AR004336	AR004336 Sequence
3	1620.5	92.8	1207	6 AR006827	AR006827 Sequence
4	1620.5	92.8	1210	6 AR031233	AR031233 Sequence

5	1620.5	92.8	1210	6	AR145049	AR145049 Sequence
6	1620.5	92.8	1989	6	AR179260	AR179260 Sequence
7	1620.5	92.8	1989	6	BD132859	BD132859 Intracell
8	1620.5	92.8	1989	6	AR282014	AR282014 Sequence
9	1620.5	92.8	8316	6	AR118703	AR118703 Sequence
10	1620.5	92.8	8987	6	AR118728	AR118728 Sequence
11	1620.5	92.8	9185	6	AR118722	AR118722 Sequence
12	1620.5	92.8	9185	6	AR118723	AR118723 Sequence
13	1620.5	92.8	9185	6	I08294	I08294 Sequence 1
14	1620.5	92.8	9185	6	BD091382	BD091382 HCV culti
15	1620.5	92.8	9379	6	AR166930	AR166930 Sequence
16	1620.5	92.8	9379	6	AR301300	AR301300 Sequence
17	1620.5	92.8	9401	6	AR176483	AR176483 Sequence
18	1620.5	92.8	9401	6	E66593	E66593 Hepatitis C
19	1620.5	92.8	9401	6	I71894	I71894 Sequence 9
20	1620.5	92.8	9401	6	I81885	I81885 Sequence 9
21	1620.5	92.8	9401	6	BD080334	BD080334 Hepatitis
22	1620.5	92.8	9401	14	HPCFLYPRE	M62321 Hepatitis C
23	1620.5	92.8	9609	12	AF387805	AF387805 Synthetic
24	1620.5	92.8	9609	12	AF387808	AF387808 Synthetic
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26	1620.5	92.8	9693	12	AF387807	AF387807 Synthetic
27	1615.5	92.5	9379	6	AR118747	AR118747 Sequence
28	1608.5	92.1	9618	14	AF271632	AF271632 Hepatitis
29	1530.5	87.7	7178	6	CQ785592	CQ785592 Sequence
30	1530.5	87.7	7178	6	CQ795334	CQ795334 Sequence
31	1530.5	87.7	7178	6	CQ867238	CQ867238 Sequence
32	1526	87.4	5125	6	AR068510	AR068510 Sequence
33	1526	87.4	5125	6	I65457	I65457 Sequence 11
34	1526	87.4	5323	6	AR068509	AR068509 Sequence
35	1526	87.4	5323	6	I65456	I65456 Sequence 9
36	1523.5	87.3	2610	14	HPCST77	M62381 Hepatitis C
37	1521.5	87.1	7551	6	CQ795336	CQ795336 Sequence
38	1521.5	87.1	7551	6	CQ867240	CQ867240 Sequence
39	1521.5	87.1	7754	6	CQ785590	CQ785590 Sequence
40	1521.5	87.1	7754	6	CQ795332	CQ795332 Sequence
41	1521.5	87.1	7754	6	CQ867236	CQ867236 Sequence
42	1521.5	87.1	9401	6	AR030378	AR030378 Sequence
43	1521.5	87.1	9416	6	AR110845	AR110845 Sequence
44	1521.5	87.1	9416	6	BD069999	BD069999 Functiona
45	1521.5	87.1	9622	6	AX663428	AX663428 Sequence

ALIGNMENTS

RESULT 1	AX154501	AX154501	Sequence 6 from Patent WO0138358.	DNA	linear	PAT 22-JUN-2001
AX154501	LOCUS	AX154501	Sequence 6 from Patent WO0138358.			
	DEFINITION	AX154501				
	ACCESSION	AX154501				
	VERSION	AX154501.1	GI:14536111			
	KEYWORDS					
	SOURCE					
	ORGANISM					
			synthetic construct			
			synthetic construct			
			other sequences; artificial sequences.			
	REFERENCE					
	AUTHORS		Selby, M. C., Glazer, E. C. and Houghton, M. C.			
	TITLE		Hbv/hcv virus-like particle			
	JOURNAL		Patent: WO 0138358-A 6 31-MAY-2001;			
			CHIRON CORPORATION (US)			
	FEATURES					
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Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 629 TGGTTCGGTGTACTCGTGGTGAATCAACTGGATTCACCAAGGTGCGGGAGCGCTCCT 688
Qy 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 689 TGTGTCTATCGAGAGGGGGGCAACACACCTGCACTGCCCCACTGATTTGCTCCGCAAG 748
Qy 231 HisProAspAlaThrTrpSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 749 CATCCGAGCGCACATCTCTCGTGGCTCCGCTCCCTGGATCACACCCAGGTGCTG 808
Qy 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 809 GTCGACTACCGGTATAGGCTTTGGCATTTATCTTTGTACCATCAACTACCATATTTAAA 868
Qy 271 IleArgMetTyrValGlyGlyValGluHisArgGlySerGlyProTrpIleThrArg 290
Db 869 ATCAGGATGTACGTGGAGGGTGCACACAGGCTGGAAGCTGCTGCAACTGGACCGG 928
Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 929 GCGGAACGTTGCGATCTGGAAGACAGGACAGGACAGGTCGCGAG 967

RESULT 3
AR006827
LOCUS AR006827 1207 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 12 from patent US 5750331.
ACCESSION AR006827
VERSION AR006827.1 GI:3966311
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1207)
AUTHORS Miyamura, T., Saito, I., Harada, S. and Honda, Y.
TITLE Diagnostic reagent for hepatitis C
JOURNAL Patent: US 5750331-A 12 12-MAY-1998;
FEATURES
Location/Qualifiers
source 1..1207
/organism="unknown"
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Alignment Scores: 1.9e-96 Length: 1207
Pred. No.: 1620.50 Matches: 283
Score: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 6 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x AR006827 (1-1207)
Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
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Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 149 GGGGGAAGTCCGGCCCACTGTGCTGGATTGTTAGCTCTCTCGCACCGGCGCAAG 208
Qy 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 209 CAGAACGTCAGCTGATCAACACACAGCGGAGTGGCACCTCAATAGCAGGCGCTGAAC 268
Qy 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90
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Db 269 TGCATATGATAGCTCAACACACCGGCTGGTTGGCAGGGCTTTTCTATCACCAAGTTCAC 328
Qy 91 SerSerGlyCysProGluAlaGlyLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 329 TCITCAGGCTGTCTCGAGAGGTAGCCAGCTGCCGACCCCTTACGATTTTTCACAGGGC 388
Qy 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 389 TGGGGCCCTATCAGTTATGCCAACCGAAGCGGCCCCGACAGCGCCCTACTGCTGGCAC 448
Qy 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 449 TACCCCCCAAAACCTTCGGTATTGTGCCGCAAGAGTGTGTGGTCCGCTATATTTCG 508
Qy 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 509 TTCACTCCAGCCCCCGTGGTGGGAACGACCGAGGTGCGGCGGCGCCACCTACAGC 568
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 569 TGGGGTGAATAATGATACGACGCTCTTCGTCTTAAACAATACCGCCACCGCTGGGCAAT 628
Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 629 TGGTTCGGTGTACTCGTGGTGAATCAACTGGATTTCAACCAAGGTGCGGAGCGCTCCT 688
Qy 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 689 TGTGTCTATCGAGAGGGGGGCAACACACCTGCACTGCCCCACTGATTTGCTCCGCAAG 748
Qy 231 HisProAspAlaThrTrpSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 749 CATCCGAGCGCACATCTCTCGTGGCTCCGCTCCCTGGATCACACCCAGGTGCTG 808
Qy 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 809 GTCGACTACCGGTATAGGCTTTGCGATTTATCTTTGTACCATCAACTACCATATTTAAA 868
Qy 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaCysAsnTrpThrArg 290
Db 869 ATCAGGATGTACGTGGAGGGTGCACACAGGCTGGAAGCTGCTGCAACTGGACCGG 928
Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 929 GCGGAACGTTGCGATCTGGAAGACAGGACAGGACAGGTCGCGAG 967

RESULT 4
AR031233
LOCUS AR031233 1210 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 35 from patent US 5866139.
ACCESSION AR031233
VERSION AR031233.1 GI:5945522
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1210)
AUTHORS Brechot, C., Krensdorf, D. and Porchon, C.
TITLE Nucleotide and peptide sequences of a hepatitis C virus isolate,
diagnostic and therapeutic applications
JOURNAL Patent: US 5866139-A 35 02-FEB-1999;
FEATURES
Location/Qualifiers
source 1..1210
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/mol_type="unassigned DNA"

ORIGIN
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Pred. No.: 1620.50 Matches: 283
Score: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
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QY	31	GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys	50
DB	167	GGGGGAAGTGGCGGCACACTGTGTGGATTGTGTAGCTCTCGCACGAGCGCAAG	226
QY	51	GlnAenValGlnLeuIleAenThrAenGlySerTrpHisLeuAenSerThrAlaLeuAen	70
DB	227	CAGAACGTCAGCTGATCAACACCGAGTGGCACCCTCAATAGCAGGCTCTGAAC	286
QY	71	CysAenAspSerLeuAenThrGlyTrpLeuAlaGlyLeuPheThrHisLysPheAen	90
DB	287	TGCNATGATAGCTTAACACCGGCTGGTGGCAGGCTTTTCTATCACCACAAGTTCAAC	346
QY	91	SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly	110
DB	347	TCTTCAGGCTGCTCAGAGGCTAGCCAGCTGCGACCCCTTACCGATTTCACGAGGC	406
QY	111	TrpGlyProIleSerTrpAlaAenGlySerGlyProAspGlnArgProTrpHis	130
DB	407	TGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGACCGGCCCTACTGCTGCAC	466
QY	131	TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys	150
DB	707	TGTGTATCGGAGGGCGGCAACACACCTGCACTGCCCTGCTGCTGCTGCTGCTGCTGCT	766
QY	231	HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu	250
DB	767	CATCCGAGCCACATACCTCTCGTGGCTCGGTCCTCGGTCCTGATCACACCCAGTGCCTG	826
QY	251	ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAenTyrThrIlePheLys	270
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UNCLASSIFIED.			
1 (bases 1 to 1210)			
Brechot,C., Kreamsdorf,D. and Porchon,C.			
Nucleotide and peptide sequences of an isolate of the hepatitis C			
virus, diagnostic and therapeutic applications thereof			
Patent: US 6210962-A 35 03-APR-2001;			
JOURNAL			
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Score:	1620.50	Matches:	283
Percent Similarity:	96.93%	Conservative:	1
Best Local Similarity:	96.59%	Mismatches:	5
Query Match:	92.81%	Indels:	4
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QY	31	GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys	50
DB	167	GGGGGAAGTGGCGGCACACTGTGTGGATTGTGTAGCTCTCGCACGAGCGCAAG	226
QY	51	GlnAenValGlnLeuIleAenThrAenGlySerTrpHisLeuAenSerThrAlaLeuAen	70
DB	227	CAGAACGTCAGCTGATCAACACCGAGTGGCACCCTCAATAGCAGGCTCTGAAC	286
QY	71	CysAenAspSerLeuAenThrGlyTrpLeuAlaGlyLeuPheThrHisLysPheAen	90
DB	287	TGCNATGATAGCTTAACACCGGCTGGTGGCAGGCTTTTCTATCACCACAAGTTCAAC	346
QY	91	SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly	110
DB	347	TCTTCAGGCTGCTCAGAGGCTAGCCAGCTGCGACCCCTTACCGATTTCACGAGGC	406
QY	111	TrpGlyProIleSerTrpAlaAenGlySerGlyProAspGlnArgProTrpHis	130
DB	407	TGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGACCGGCCCTACTGCTGCAC	466
QY	131	TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys	150
DB	467	TACCCCCCAAACTTGGCGTATTGTGCCGGAAGAGTGTGTGCTCGGTATATTGC	526
QY	151	PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer	170
DB	527	TTCACTCCCGAGCCCGTGGTGGGAACGACGACGAGTGGCGCGGCCCTACACG	586
QY	171	TrpGlyGluAenAspThrAspValPheValLeuAenAenThrArgProLeuGlyAen	190
DB	587	TGGGGTGAATAATGATACGAGCTTCTGCTTAAACATACGAGGCCACCGCTGGGCAAT	646
QY	191	TrpPheGlyCysThrTrpMetAenSerThrGlyPheThrLysValCysGlyAlaProPro	210
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QY	211	CysValIleGlyAlaGlyAlaGlyAenAenThrLeuHisCysProThrAspCysPheArgLys	230
DB	707	TGTGTATCGGAGGGCGGCAACACACCTGCACTGCCCTGCTGCTGCTGCTGCTGCTGCT	766
QY	231	HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu	250
DB	767	CATCCGAGCCACATACCTCTCGTGGCTCGGTCCTCGGTCCTGATCACACCCAGTGCCTG	826
QY	251	ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAenTyrThrIlePheLys	270
DB	827	GTGCACTACCCGCTATAGGCTTTGGCATTATCTTGTACCATCAACTACACCATATTTAAA	886
QY	271	IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAenThrTrpThrArg	290
DB	887	ATCAGGATGTACGTGGAGGGTGGAAACACAGGCTGGAAAGCTGCCCTGCAACTGGACGCG	946
QY	291	GlyGluArgCysAspLeuGluAspArgAspArgSerGlu	303
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DEFINITION	Sequence 35 from patent US 6210962.		
ACCESSION	AR145049		
VERSION	AR145049.1 GI:15106916		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		



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 LOCUS Sequence 4 from patent US 6326171.  
 DEFINITION ARI79260  
 ACCESSION ARI79260  
 VERSION ARI79260.1 GI:20220815  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 1989)  
 AUTHORS Selby, M. and Houghton, M.  
 TITLE Hepatitis C E1 and E2 truncated polypeptides and methods of obtaining the same  
 JOURNAL Patent: US 6326171-A 4 04-DEC-2001;  
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 Pred. No.: 1620.50 Matches: 283  
 Score: 96.93% Conservative: 1  
 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: 6 Gaps: 1  
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 Db 256 TCTTACGCTGCTCTGAGAGGCTAGCAGCTGCGGACCCCTTACCAGATTGTCACAGGGC 315  
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 Db 316 TGGGGCCCTATCATGTTATGCTCAACGGAAGCGGCCCGCCCTACTCTGGCAC 375  
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 QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
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Db 496 TGGGGTGAAATGATACGGACGCTTCTCGTCTTAACAATACCAAGCCACCGCTGGGCAAT 555  
 QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
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 Db 556 TGGTTCGGTTGTATACCTGGATGAACCTCAACTGGATTCCACAAAGTGTCCGAGCGCCCTCT 615  
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 QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
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 QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnThrIlePheLys 270  
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 Db 736 GTCGACTACCGGTATAGGCTTTGGCATTATCTTGTACCATCACTACATATATTTAAA 795  
 QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
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 Db 796 ATCAGGATGTACGTGGAGGGGTCGAGACAGAGCTGGAGCTGCTGCACTGGACGCG 855  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspSerGlu 303  
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 Db 856 GCGAAGCTTTCGATCTGGAAGATAGGACAGGTCCGAG 894  
 RESULT 7  
 BD132859 1989 bp DNA linear PAT 18-SEP-2002  
 LOCUS Intracellular production of hepatitis C E1 and E2 truncated polypeptides.  
 DEFINITION BD132859  
 ACCESSION BD132859  
 VERSION GI:23227804  
 KEYWORDS JP 2002504810-A/2.  
 SOURCE unidentified  
 ORGANISM unidentified  
 REFERENCE 1 (bases 1 to 1989)  
 AUTHORS Houghton, M., Choo, Q. L., Abrignani, S., Chien, D., Selby, M. and Glazer, S.  
 TITLE Intracellular production of hepatitis C E1 and E2 truncated  
 JOURNAL Patent: JP 2002504810-A 2 12-FEB-2002;  
 COMMENT CHIRON CORP  
 OS Hepatitis virus (hepatitis C virus)  
 PN JP 2002504810-A/2  
 PD 12-FEB-2002  
 PF 06-MAY-1998 JP 1998548360  
 PR 06-MAY-1997 US 60/045675  
 PI MICHAEL HOUGHTON, QUI LIM CHOO, SERGIO ABRIGNANI, DAVID CHIEN, MARK SELBY,  
 EDWARD GLAZER  
 PC C12N15/40, C07K14/18, A61K39/29, G01N33/50  
 CC  
 FH Key Location/Qualifiers  
 FT CDS Location/Qualifiers  
 source 1..1989  
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 Alignment Scores: 3.23e-96 Length: 1989  
 Pred. No.: 1620.50 Matches: 283  
 Score: 96.93% Conservative: 1  
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 Query Match: 92.81% Indels: 5  
 DB: 6 Gaps: 1  
 US-10-715-665-7\_COPY\_1\_303 (1-303) x BD132859 (1-1989)



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Db 796 ATCAGGATGTACGTGGAGGGGTGGAACACAGCGTGGAGGCTGCTGCAACTGGACGCG 855
QY 291 GlyGluArgCysAspLeuGluAspArgSerGlu 303
Db 856 GCGACGTTGCGATCTGGAAGATAGGACAGGTCGAG 894

RESULT 9
AR118703
LOCUS AR118703 8316 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 88 from patent US 6150087.
ACCESSION AR118703
VERSION AR118703.1 GI:14100613
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 8316)
AUTHORS Chien,D.Y.
TITLE NANBV diagnostics and vaccines
JOURNAL Patent: US 6150087-A 88 21-NOV-2000;
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1..48e-95 Length: 8316
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 6 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x AR118703 (1-8316)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 778 GTGCTGCTGCTATTGCGCGGCTC-----GACGCGGAAACCCACGTCACC 822
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 823 GGGGGAAGTGGCGGCGCACACTGTGTCTGGATTGTTAGCTCTCTCGCACGCGCAAG 882
QY 51 GlnAsnValGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 70
Db 883 CAGAACGTCAGCTGATCAACACACAGCGAGTTGGACCTCAATAGCAGCGCCCTGAAC 942
QY 71 CysAsnAspSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 90
Db 943 TGCATGATAGCTCAACACCGGCTGTTGGCAGGCTTTTCTATCACCAAGTTCAAC 1002
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1003 TCTTTCAGGCTGCTCCTGAGAGGCTAGCAGCTGCGGACCGCCCTTACCAGATTTCACCAAGGC 1062
QY 111 TrpGlyProLeuSerTyrrAlaAsnGlySerGlyProAspGlnArgProTyrrCysTrpHis 130
Db 1063 TGGGGCCCTATCAGTTATGCCAACGAGCGGCGCCCGACGAGCGCCCTACTGCTGGCAC 1122
QY 131 TyrProProLysProCysGlyLeuValProAlaLysSerValCysGlyProValTyrrCys 150
Db 1123 TACCCCCCAAAACCTTGGCGTATTGTCGCGGAGAGTGTGTGGTCCGGTATATTGC 1182
QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrrSer 170
Db 1183 TTCACCTCCAGCCCGCTGTGGTGGGAACGACGACGAGTGGCGCGCCACCTACAGC 1242
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1243 TGGGGTGAATATGATACGACGCTCTTCGTCCTTAACATACAGGCCACCGCTGGGCAAT 1302
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
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Db 1303 TGGTTCGGTGTACCTGGATGAACCTCACTGGATTCAACAAAGTGTGGGAGCGCTCCT 1362
QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 1363 TGTGTCTATCGAGGGGCGGCAACACACCTGCTACTGCCCCACTGATTGCTTCCGCAAG 1422
QY 231 HisProAspAlaThrTyrrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 1423 CATCCGAGCGCCACATACTCTCGGTGCGGCTCCGTCCTGGATCAACACCGAGTGGCTG 1482
QY 251 ValAspTyrrProTyrrArgLeuTrpHisTyrrProCysThrIleAsnTyrrThrIlePheLys 270
Db 1483 GTCGACTACCGGTATAGGCTTTGGCATTTATCTTGTACCATCACTACACCATATTATAA 1542
QY 271 IleArgMetTyrrValGlyGlyValGluHisArgLeuGluAlaCysAsnTrpThrArg 290
Db 1543 ATCAGGATGTACGTGGAGGGGTGGAACACAGCTGGAAGCTGCCTGCAACTGGACGCG 1602
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 1603 GCGCAACGTTGCGATCTGGAACAGGACAGGACAGGTCGCGAG 1641

RESULT 10
AR118728
LOCUS AR118728 8987 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 137 from patent US 6150087.
ACCESSION AR118728
VERSION AR118728.1 GI:14100638
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 8987)
AUTHORS Chien,D.Y.
TITLE NANBV diagnostics and vaccines
JOURNAL Patent: US 6150087-A 137 21-NOV-2000;
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 1..6e-95 Length: 8987
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 6 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x AR118728 (1-8987)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
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QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 1165 GGGGGAAGTGGCGGCGCACACTGTGTCTGGATTGTTAGCTCTCTCGCACGAGCGCAAG 1224
QY 51 GlnAsnValGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 70
Db 1225 CAGAACGTCAGCTGATCAACACACGCGAGTTGGCAGCTCAATAGCAGCGCCCTGAAC 1284
QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrrHisHisLysPheAsn 90
Db 1285 TGCATGATAGCTCAACACCGGCTGTTGGCAGGCTTTTCTATCACCAAGTTCAAC 1344
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1345 TCTTCAGGCTGCTCCTGAGAGGCTGCCAGCTCCGACCCCTTACCGATTTCACGAGGC 1404
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QY 111 TtpGlyProIleSerTyrAlaIleGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
 DB 1405 TGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGACAGCGCCCTTACTGTGGCAC 1464  
 QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
 DB 1465 TACCCCCAAAACCTTGGCGTATTGTGCCCGGGAAGAGTGTGTGGTCCGGTATATTGC 1524  
 QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
 DB 1525 TTCACTCCCGAGCCCGTGGTGGGACAGCAGCAGTCCGGCGGCCACCTACAGC 1584  
 QY 171 TtpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
 DB 1585 TGGGGTGAATATGATACGAGCTTTCGTCCTTAAACATACCAGGCCACCGCTGGGCAT 1644  
 QY 191 TtpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
 DB 1645 TGGTTCGGTGTACCTGGATGAACCACTGGATTACCAAGTGTGGGAGCGCTCCT 1704  
 QY 211 CysValIleGlyCysGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
 DB 1705 TGTGTATCGAGGGCGGCGCAACACACCTGCACTGCCACCTGATTGCTTCCGCAAG 1764  
 QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 DB 1765 CATCCGGAGCCACATACATCTCTGGTGGCTCCGGTCCCTGGATACACCCAGGTGCC 1824  
 QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 DB 1825 GTCCACTACCCGTATAGCTTTGGCATATCTTGTACCATCAACTACACCATATTAAA 1884  
 QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
 DB 1885 ATCAGGATGTAGCTGGGAGGGTGGAAACACAGCTGGAAGCTGCCCTGCAACTGGAC 1944  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 DB 1945 GCGCAACGTTGGATCTGGAAGACAGGACAGTCCGAG 1983

RESULT 11  
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 LOCUS AR118722 9185 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 122 from patent US 6150087.  
 ACCESSION AR118722  
 VERSION AR118722.1 GI:14100632  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 Chien, D.Y.  
 TITLE NANBV diagnostics and vaccines  
 JOURNAL Patent: US 6150087-A 122 21-NOV-2000;  
 FEATURES Location/Qualifiers  
 source 1..9185  
 /organism="unknown"  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 1,64e-95 Length: 9185  
 Score: 1620.50 Matches: 283  
 Percent Similarity: 96.93% Conservative: 1  
 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: 6 Gaps: 1  
 US-10-715-665-7\_COPY\_1\_303 (1-303) x AR118722 (1-9185)  
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 DB 1439 GTGCTGCTGCTATTTCGGCGCTC-----GACGCGAAACCCACGTCACC 1483

QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
 DB 1484 GGGGGAAGTGGCGCCACACTGTGTGATTTGTAGCTCTCGACAGGCCCGCAAG 1543  
 QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
 DB 1544 CAGAACGTCCAGCTGATCAACACACCGCAGTTGGCACCTCAATAGCACGSCCTGAAC 1603  
 QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90  
 DB 1604 TGCAATGATAGCTCAACACCGCTGGTGGCAGGCTTTCTATCACCACCAAGTTCAAC 1663  
 QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
 DB 1664 TCTTCAGGCTGTCTGAGAGGCTAGCAGCTGCCACCCCTTACCAGATTTTGACACGAGC 1723  
 QY 111 TtpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
 DB 1724 TGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGACAGCGCCCTTACTGTGGCAC 1783  
 QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
 DB 1784 TACCCCCAAAACCTTGGCGTATTGTGCCCGCAAGAGTGTGTGGTCCGGTATATTGC 1843  
 QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
 DB 1844 TTCATCCCGAGCCCGTGGTGGAAACGACAGCTCGGGCGGCCACCTACAGC 1903  
 QY 171 TtpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
 DB 1904 TGGGGTGAATATGATACGAGCTTTCGTCCTTAAACATACCAGGCCACCGCTGGGCAAT 1963  
 QY 191 TtpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
 DB 1964 TGGTTCGGTGTGTACCTGGATCAACTGGATTCACCAAGTGTGGGAGCGCTCCT 2023  
 QY 211 CysValIleGlyGlyValGlyValGluHisCysProThrAspCysPheArgLys 230  
 DB 2024 TGTGTATCGGAGGGCGGCAACACACCTTGCACTGCCCGCTGATTTGCTTCGCAAG 2083  
 QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 DB 2084 CATCCGGAGCCACATACCTCTCGGTGGCTCCGCTCCCTGGATCACACCCAGGTGCCTG 2143  
 QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 DB 2144 GTCGACTACCCGCTATAGGCTTTGGCATTTATCCTTGTACCATCAACTACACCATATTAAA 2203  
 QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
 DB 2204 ATCAGGATGTAGTGGGAGGGTGGAAACACAGCTGGAGAGCTGCTGCNACTGGACGCG 2263  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 DB 2264 GCGCAACGTTGGATCTGGAAGACAGGACAGTCCGAG 2302

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 LOCUS AR118723 9185 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 123 from patent US 6150087.  
 ACCESSION AR118723  
 VERSION AR118723.1 GI:14100633  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 Chien, D.Y.  
 TITLE NANBV diagnostics and vaccines  
 JOURNAL Patent: US 6150087-A 123 21-NOV-2000;  
 FEATURES Location/Qualifiers  
 source 1..9185





Score: 1620.50 Matches: 283  
Percent Similarity: 96.93% Conservative: 1  
Best Local Similarity: 96.59% Mismatches: 4  
Query Match: 92.81% Indels: 5  
DB: 6 Gaps: 1

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Qy	11	ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr	30
Db	1439	GTGCTGCTGCTATTTCGGCGGTC-----GACGGGAAACCCACGTCACC	1483
Qy	31	GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys	50
Db	1484	GGGGGAAGTCGGCCACACACTGTGCTGGATTGTAGCCTCTCGCACCAGGCGCAAG	1543
Qy	51	GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn	70
Db	1544	CAGAACGTCAGCTGATCAACACACCGGAGTGGCACCTCAATAGCAGGCGCCCTGAAC	1603
Qy	71	CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn	90
Db	1604	TGCAATGATAGCTTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCAAGTTCAAC	1663
Qy	91	SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly	110
Db	1664	TCTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCGCAGCCCTTACCGATTTTGACCAAGGC	1723
Qy	111	TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis	130
Db	1724	TGGGGCCCTATCAGTTATGTCACCGAAGCGGCCCGCCAGCCGCTACTGCTGGCAC	1783
Qy	131	TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys	150
Db	1784	TACCCCAAAACCTTGGCGTATTGTGCCCGCGAAGAGTGTGTGGTCCGGTATATTGC	1843
Qy	151	PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer	170
Db	1844	TTCACTCCCAAGCCCGTGGTGGGAAACGACCGACAGGTGCGGCGCGCCACTACAGC	1903
Qy	171	TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn	190
Db	1904	TGGGGTGAAATGATACGGACGTCTTCGTCTTTAACAATACCGAGCCACCGCTGGGCAAT	1963
Qy	191	TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro	210
Db	1964	TGTTTCGGTTGTACCTGGATGAACCTCACTGGATTCAACCAAGTGTGGGAGCGCTCCT	2023
Qy	211	CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys	230
Db	2024	TGTGTCACTCGAGGGCGGGCAACACACCTGCCTGCCTGCCCACTGATTGCTTCCGCAAG	2083
Qy	231	HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu	250
Db	2084	CATCCGGAGCCACATACTCTCGGTGGGCTCCGGTCCCTGGATCAACCCAGGTGCTG	2143
Qy	251	ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys	270
Db	2144	GTGCACTACCCGTATAGGCTTTGGCATTTATCTTTGACCATCACTACCATATTATAA	2203
Qy	271	IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg	290
Db	2204	ATCAGGATGTACGTGGAGGGGTGAAACACAGGCTGGAGCTGCCTGCAACTGGACGCGG	2263
Qy	291	GlyGluArgCysAspLeuGluAspArgAspArgSerGlu	303
Db	2264	GGCGAACGTTGCATCTGGAAGACAGGGACAGGTCCGAG	2302

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Run on: April 15, 2005, 02:41:03 ; Search time 611 Seconds  
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Title: US-10-715-665-7\_COPY\_1\_303

Perfect score: 1746

Sequence: 1 MDAMKGLCCVLLCGAVFV.....AACNWTGRGCDLEDRDSE 303

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: Geneseq\_2003cs.\*

11: Geneseq\_2003ds.\*

12: Geneseq\_2004as.\*

13: Geneseq\_2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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5	92.8	1914	8	ACC71824	Acc71824 HCV-1 E1/
92.8	1914	12	ADO00769	Ado00769 HCV-1 E1/	

6	1620.5	92.8	1989	2	AAT18246	Aat18246 HCV1 E2/N
7	1620.5	92.8	1989	2	AAV81371	Aav81371 Hepatitis
8	1620.5	92.8	8316	2	AAQ05955	Aaq05955 Hepatitis
9	1620.5	92.8	8316	3	AAV52396	Aav52396 cDNA sequ
10	1620.5	92.8	8316	12	ADN35977	Adn35977 HCV cDNA
11	1620.5	92.8	9185	2	AAQ05956	Aaq05956 Sense str
12	1620.5	92.8	9185	2	AAQ10566	Aaq10566 Hepatitis
13	1620.5	92.8	9185	2	AAQ00459	Aaq00459 Hepatitis
14	1620.5	92.8	9185	2	AAV26737	Aav26737 Nucleotid
15	1620.5	92.8	9185	2	ADF66068	Adf66068 Hepatitis
16	1620.5	92.8	9185	3	AAV5297	Aav5297 Sense str
17	1620.5	92.8	9400	2	AAQ21744	Aaq21744 Compiled
18	1620.5	92.8	9401	2	AAQ12170	Aaq12170 Hepatitis
19	1620.5	92.8	9401	2	AAV99981	Aav99981 HCV poly
20	1620.5	92.8	9401	2	AAV09989	Aav09989 HCV poly
21	1620.5	92.8	9401	6	AAQ35043	Aaq35043 Hepatitis
22	1620.5	92.8	9401	12	ADL23106	Adl23106 Hepatitis
23	1620.5	92.8	9401	13	ADR29358	Adr29358 Hepatitis
24	1617.5	92.6	9185	12	ADN35979	Adn35979 HCV cDNA
25	1612.5	92.4	9379	2	AAQ36209	Aaq36209 Composite
26	1608.5	92.1	9618	11	ADN33102	Adn33102 Hepatitis
27	1580.5	90.5	9133	2	AAZ07656	Aaz07656 Nucleotid
28	1530.5	87.7	7178	12	ADL72979	Adl72979 Hepatitis
29	1526	87.4	5125	2	AAQ47196	Aaq47196 Plasmid p
30	1526	87.4	5323	2	AAQ47195	Aaq47195 Plasmid p
31	1523.5	87.3	1207	2	AAQ40331	Aaq40331 Sequence
32	1521.5	87.1	7551	12	ADL72981	Adl72981 Hepatitis
33	1521.5	87.1	7754	12	ADL72977	Adl72977 Hepatitis
34	1521.5	87.1	9401	2	AAV41882	Aav41882 Hepatitis
35	1521.5	87.1	9416	2	AAV59378	Aav59378 Hepatitis
36	1521.5	87.1	9416	6	ABK87300	Abk87300 cDNA enco
37	1521.5	87.1	9416	8	ACA62483	Acac62483 HCV-H CDN
38	1521.5	87.1	9622	10	AAV54424	Aav54424 Hepatitis
39	1518.5	87.0	9365	6	AAZ25518	Aaz25518 Hepatitis
40	1515.5	86.8	9646	2	AAV59361	Aav59361 Hepatitis
41	1515.5	86.8	9646	6	ABK87285	Abk87285 cDNA enco
42	1515.5	86.8	9646	8	ACA62466	Acac62466 HCV H77 c
43	1515.5	86.8	11674	3	AAZ36210	Aaz36210 Nucleotid
44	1515.5	86.8	12980	2	AAV59364	Aav59364 Hepatitis
45	1515.5	86.8	12980	6	ABK87286	Abk87286 Hepatitis

## ALIGNMENTS

RESULT 1

AAD06793

ID AAD06793 standard; DNA; 5882 BP.

XX AAD06793;

XX 06-AUG-2001 (first entry)

XX Plasmid pCMV-II-E2661-SAG.

XX Virus-like particle; immunogen; hepatitis B virus surface antigen; HBsAg;

XX HBV; chimeric antigen; hepatitis C virus; HCV; virucide; vaccine;

XX plasmid pCMV-II-E2661-SAG; cyclic; circular; ds.

XX Human cytomegalovirus.

XX Homo sapiens.

XX Hepatitis C virus.

XX Hepatitis B virus.

XX Bos sp.

XX Unidentified.

XX Chimeric.

XX Key

XX Location/Qualifiers

FT CDS

FT /tag= a

FT /product= "HCV 661 E2 envelope glycoprotein-HBsAg S

FT domain"

FT misc\_feature

FT 1992..2900

FT /\*tag= b

FT	misc_feature	/note= "661 E2 coding sequence from HCV"
FT	FT	2907..3587
FT	FT	/*tag= C
FT	FT	/note= "HBsAg S domain coding sequence from HBV"
XX		
XX	WO200138358-A2.	
XX		
XX	31-MAY-2001.	
XX		
XX	22-NOV-2000; 2000WO-US032249.	
XX		
XX	24-NOV-1999; 99US-0167224P.	
XX		
FA	(CHIR ) CHIRON CORP.	
XX		
PI	Selby M, Glazer E, Houghton M;	
XX		
XX	WPI: 2001-367661/38.	
DR	P-PSDB; RAE02622.	
XX		
PT	Virus-like particle for use as an immunogen, comprising a first hepatitis B virus surface antigen (HBsAg) and chimeric antigen comprising a second HBsAg covalently linked to hepatitis C immunogenic polypeptide.	
PT		
XX		
PS	Claim 37; Fig 4; 115pp; English.	
XX		
CC	The invention relates to a virus-like particle for use as an immunogen, comprising a first hepatitis B virus surface antigen (HBsAg) and a chimeric antigen comprising a second HBsAg which is covalently linked to an hepatitis C virus (HCV) immunogenic polypeptide, where the first and the second HBsAg each comprise a substantially complete S domain. The virus-like particle is useful as immunogen and as vaccing. The present sequence is plasmid pCMV-II-E2661-sag containing coding sequences for 661 E2 envelope glycoprotein of HCV and S domain of HBsAg inserted into pCMVII. The plasmid pCMVII is a pUC19-based cloning vector designed for expression in mammalian cells. It comprises human cytomegalovirus (CMV) immediate early (IE) enhancer/promoter, human CMV intron A, a human tissue plasminogen activator (tPA) leader, a bovine growth hormone poly A terminator (BGHT), a ColEI origin of replication and an ampicillin resistance (Amp R) gene. The pCMV-II-E2661-sag plasmid is used for production of virus-like particle of the invention	
XX		
XX	Sequence 5882 BP; 1378 A; 1543 C; 1469 G; 1492 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	2,96e-119	Length: 5882
Score:	1746.00	Matches: 303
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	5	Gaps: 0
US-10-715-665-7_COPY_1_303 (1-303) x AAD06793 (1-5882)		
Qy	1	MetAspAlaMetLysArgGlyLeuCysCysValIleuLeuLeuLeuLeuValPheVal 20
Db	1992	ATGATGCAATGAAGAGAGAGGCTCTGCTGTGCTGTGCTGTGCTGTGAGCAGTCTTCGT 2051
Qy	21	SerProSerAlaSerGluThrHisValThrGlyGlySerAlaGlyHisThrValSerGly 40
Db	2052	TCGCCACAGCGGTACGGAACCCACGTCACCGGGGGAAGTGC CGGCCACACCTGTGTCTGGA 2111
Qy	41	PheValSerLeuLeuAlaProGlyAlaLysGlnAsnValGlnLeuLeuAsnThrAsnGly 60
Db	2112	TTTGTGTAGCTTCCTCGACACAGGCGCCAAAGCAGACAGCTCCACGTGATCAACACCAACGGC 2171
Qy	61	SerTrpHisLeuAsnSerThrAlaLeuAsnCysAsnAspSerLeuAsnThrGlyTrpLeu 80
Db	2172	AGTTGGCACCTCAATAGCACGGCCCTGAACCTGCAATGATACCTCAACACCGCTGGTGT 2231
Qy	81	AlaGlyLeuPheTrpHisHisLysPheAsnSerSerGlyCysProGluArgLeuAlaSer 100
Db	2232	GCAGGGCTTTCTATCACCAAGTTCACCTCTTCAGGCTGTCTGTGAGAGCTAGCCAGC 2291

PA (NAHE-) NAT INST OF HEALTH.  
 XX Miyamura T, Saito I, Harada S, Honda Y;  
 XX WPI; 1993-127516/16.  
 DR P-PSDB; AAR34438.  
 XX  
 PT Diagnostic reagent for hepatitis C virus - comprises second envelope  
 PT protein or first non-structural protein encoded by HCV gene and has sugar  
 PT chain.  
 XX  
 XX Claim 8; Page 30-32; 58pp; English.  
 XX  
 CC Glycoprotein E2/NS1 is derived from the second envelope protein or first  
 CC non-structural protein encoded by the genome of HCV. The nucleic acid is  
 CC extracted from the serum of the patient of hepatitis C. The serum is  
 CC pref. mixed with transfer RNA (tRNA) as a carrier of virus RNA. As a  
 CC technique of cloning cDNA from the nucleic acid, it is preferred to use  
 CC polymerase chain reaction method. In the reaction, any commercially  
 CC available random primers or synthesized DNA having a base sequence  
 CC similar to that of primer AS1 may be used as a primer. Representative  
 CC examples of sense primers include S1. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX

SQ Sequence 1207 BP; 241 A; 369 C; 336 G; 261 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8.91e-111 Length: 1207  
 Score: 1620.50 Matches: 283  
 Percent Similarity: 96.93% Conservative: 1  
 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: 2 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x AAQ40330 (1-1207)

Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
 Db 104 GTGCTGCTGCTATTGGCGGCTC-----GACGGGAAACCCACGTCACC 148  
 Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
 Db 149 GGGGGAAGTGGCGGCAACACGTCGTGGATTGTTAGCTCTCGCCACGAGGCGCAAG 208  
 Qy 51 GlnAsnValGlnLeuLeuLeuAsnThrAsnGlySerTrpHisLeuLeuAsnThrAlaLeuAsn 70  
 Db 209 CAGAACCTCCAGCTGATCNACACCAACGCGAGTTGGCACCTCAATACACGCGCTCAAC 268  
 Qy 71 CysAsnAspSerLeuLeuLeuAsnThrGlyTrpLeuAlaGlyLeuPheTrpHisPheAsn 90  
 Db 269 TGCAATGATAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACCAAGTTCAAC 328  
 Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
 Db 329 TCITTCAGGCTGCTCAGAGCTAGCAGCTGCGCGCCGCGCCCTTACCGATTGACCGAGGC 388  
 Qy 111 TrpGlyProIleSerTrpAlaAsnGlySerGlyProAspGlnArgProTrpCysTrpHis 130  
 Db 389 TGGGCGCTTATCAGTTATGCAACGGAAGCGGCGCCCGACCGCGCCCTTACTGCTGGCAC 448  
 Qy 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
 Db 449 TACCCCGCAAAACCTTCGGTATTGTCGCGGGAAGAGTGTGTGTCGCGGTATATTGC 508  
 Qy 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTrpSer 170  
 Db 509 TTCACTCCAGCCCCGTTGGTGGGAACCAACCGAGGTGGGCGGCCCGCCACTACAGC 568  
 Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuLeuAsnAsnThrArgProProLeuGlyAsn 190  
 Db 569 TGGGGTGAATATGATACGAGCGCTTCGTCTTAAACAATACCGACCGCCGCTGGGCAAT 628  
 Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210

Db 629 TGGTTCGGTTGTACCTGGATGAACCTCACTGGATTCAACAAAGTGTGCGAGCGCTCCT 688  
 Qy 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
 Db 689 TGTGTCTATCGAGGGGGGCAACACACCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 748  
 Qy 231 HisProAspAlaThrTrpSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 Db 749 CATCCGAGCGCCACATACCTCTCGGTGGGCTCGGTCTCGGTCTCGGTCTCGGTCTCG 808  
 Qy 251 ValAspTyrProTrpArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 Db 809 GTCCACTACCGTATAGCTTTGGCATTTATCTTGTACCATCACTACCATATTTAAA 868  
 Qy 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
 Db 869 ATCAGGATGTACGTGGGAGGGGTGCAACACAGGTGGAAGTGGCTGCTGCTGCTGCTG 928  
 Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 Db 929 GCGGAACGTTGCGATCTGGAAGACAGGACAGGACAGGACAGGACAGGACAGGACAG 967

RESULT 3

ABZ70946

ID ABZ70946 standard; DNA; 1914 BP.

XX AC ABZ70946;

XX DT 23-APR-2003 (first entry)

XX DE Hepatitis C virus E1/E2/p7 region protein encoding DNA SEQ ID NO:3.

XX KW Hepatitis C virus; HCV; E1E2 antigen; vaccine; immune response;

XX XW submicron oil-in-water emulsion; immunostimulatory; virucide; vaccine;

XX XW gene; ds.

XX OS Hepatitis C virus.

XX FH Key Location/Qualifiers

XX FT CDS 1..1914

XX FT /\*tag= a

XX FT /partial

XX FT /product= "E1/E2/p7 region protein"

XX FT /note= "no start codon given"

XX PN W02003002065-A2.

XX XX 09-JAN-2003.

XX XX 28-JUN-2002; 2002WO-US020676.

XX XX 29-JUN-2001; 2001US-0302227P.

XX XX (CHIR ) CHIRON CORP.

XX XX Houghton M, Coates SR, O'hagan D;

XX XX WPI; 2003-247904/24.

XX XX P-PSDB; ABP57410.

XX XX Novel hepatitis C virus E1E2 vaccine composition for stimulating an

XX XX immune response in a vertebrate, comprises E1E2 antigens, submicron oil-

XX XX in-water emulsions and/or CpG oligonucleotides.

XX XX Claim 3; Fig 2A-C; 69pp; English.

XX XX The present invention describes a composition (I) comprising a hepatitis

XX XX C virus (HCV) E1E2 antigen and a submicron oil-in-water emulsion that

XX XX lacks N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2- (1'-2'-

XX XX dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), where

XX XX the submicron oil-in-water emulsion is capable of enhancing the immune

XX XX response to the HCV E1E2 antigen and/or an immunostimulatory nucleic acid



XX SQ Sequence 1914 BP; 349 A; 590 C; 535 G; 440 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-54e-110	Length:	1914
Score:	1620.50	Matches:	283
Percent Similarity:	96.93%	Conservative:	1
Best Local Similarity:	96.59%	Mismatches:	4
Query Match:	92.81%	Indels:	5
DB:	8	Gaps:	1

US-10-715-665-7\_COPY\_1\_303 (1-303) x ACC71824 (1-1914)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30

Db 604 GTGCTGCTGCTATTGGCGGCTC-----GAGCGGAAACCCACGTCACC 648

QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50

Db 649 GGGGGAAGTCCGGCCACACTGTGTCTGGATTGTTAGCCTCTCGCACCAGGCGCAAG 708

QY 51 GluAsnValGlnLeuLeuLeuAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70

Db 709 CAGAACGTCAGCTGATCAACACACGAGGAGTTGGCACCTCAATACGAGGCTTCAAC 768

QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90

Db 769 TGAATGATAGCTCAACACCGGCTGTTGGCAGGCTTTTCTATCACCAACAGTTCAAC 828

QY 91 SerSerGlyCysProGluAlaGluLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110

Db 829 TCTTCAGGCTGTCTGAGAGCTAGCCAGCTGCGACCCCTTACCGATTGACAGGCG 888

QY 111 TrpGlyProLysSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130

Db 889 TGGGCGCCTATCAGTTATGCAACGGAAGCGGCCCGCCAGCGCCCTACTGCTGGCAC 948

QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150

Db 949 TACCCCAAAACCTTCGCGGTATTGTGCCCGCGAAGAGTGTGTGCTCGGTATATTGC 1008

QY 151 PheThrProSerProValValValGlyThrAspArgSerGlyAlaProThrTyrSer 170

Db 1009 TTCACCTCCACGCCCCGCTGGTGGGAACGACGACAGGTGCGGCGCGCCACCTACAGC 1068

QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyVal 190

Db 1069 TGGGTGAAATGATACGGACGCTTCTGCTCTTAACAAATACAGCCCGCCGCTGGGCAAT 1128

QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210

Db 1129 TGGTTCGGTTGTACCTGGATGAATCACTCACTGGATTACCAAGGTGCGGAGCGCTCCT 1188

QY 211 CysValIleGlyAlaGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230

Db 1189 TGTGTATCATCGAGGCGGGGCAACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1248

QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250

Db 1249 CATCCGACCCACATACCTCTCGGTGGGCTCGGCTCCGCTGATACACCGAGTGCCTG 1308

QY 251 ValAspTyrProTyrArgLeuThrHisTyrProCysThrIleAsnTyrThrIlePheLys 270

Db 1309 GTGACGTACCGTATAGCTTTGGCATATCTTGTACCATCACTACATATATTAA 1368

QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaCysAsnTrpThrArg 290

Db 1369 ATCAGGATGTACGTGGAGGGGTGAGACAGGCTGGAAGCTGCTGCACTGGAGCGG 1428

QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303

Db 1429 GCGCAAGTGTGCGATCTGGAAGATAGGAGCAGGTCCGAG 1467

RESULT 5

ADO00769

ID ADO00769 standard; DNA; 1914 BP.

XX AC ADO00769;

XX AC ADO00769;

XX DT 29-JUL-2004 (first entry)

XX DE HCV-1 E1/E2/p7 region nucleotide sequence SEQ ID NO:3.

XX KW fusion protein; hepatitis C virus; HCV; NS3; NS4; core polypeptide;

XX KW polypeptide; HCV-1; antiviral; vaccine; T cell activation;

XX OS E1/E2/p7 region; gene; ds; NS5.

XX OS Hepatitis C virus.

PH Key Location/Qualifiers

FT CDS 1..1914

FT /\*tag= a

FT /product= "HCV-1 E1/E2/p7 region"

XX WO2004039950-A2.

XX PD 13-MAY-2004.

XX PF 24-OCT-2003; 2003WO-US033610.

XX PR 25-OCT-2002; 2002US-00281341.

XX PA (CHIR ) CHIRON CORP.

XX PI Houghton M, Coates S, Selby M, Paliard X;

XX WI; 2004-376177/35.

XX P-PSDB; ADO00770.

XX New fusion protein comprises hepatitis C virus (HCV) polypeptides, which consist of an NS3, an NS4, an NS4 and a core polypeptide of HCV, useful for stimulating immune response, e.g. activating T cells of a vertebrate.

XX Disclosure; SEQ ID NO 3; 136pp; English.

XX The present invention describes a fusion protein comprising hepatitis C virus (HCV) polypeptides, where the HCV polypeptides consist of an NS3, an NS4, an NS5 and a core polypeptide of HCV, and the core polypeptide consist of amino acids 1-121 of the HCV polypeptide, numbered relative to the full-length HCV-1 polypeptide. Also described: (1) an isolated and purified polynucleotide that encodes the fusion protein; (2) a composition comprising the fusion protein or the isolated and purified polynucleotide and a pharmaceutical excipient; and (3) activating T cells of a vertebrate subject which recognise an epitope of an HCV polypeptide. The fusion protein has antiviral activity, and can be used in vaccines. The composition is useful for activating T cells of a vertebrate subject which recognise an epitope of an of the NS3, NS4, NS5 and/or core polypeptides. It is also useful for the manufacturing of a medicament for activating T cells. The present sequence encodes an HCV-1 E1/E2/p7 region amino acid sequence, which is used in the exemplification of the present invention.

XX SQ Sequence 1914 BP; 349 A; 590 C; 535 G; 440 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-54e-110	Length:	1914
Score:	1620.50	Matches:	283
Percent Similarity:	96.93%	Conservative:	1
Best Local Similarity:	96.59%	Mismatches:	4
Query Match:	92.81%	Indels:	5
DB:	12	Gaps:	1

US-10-715-665-7\_COPY\_1\_303 (1-303) x ADO00769 (1-1914)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30

Db 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30

Db 604 GTGCTGCTGCTATTTTCCGGCGTC-----GACGCGGAAACCCACGTCAC 648  
 QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
 Db 649 GGGGGAAGTCCGGCCACACTGTGTCTGGATTGTGTAGCTCTCGCACAGCGCCAA 708  
 QY 51 GlnAsnValGlnLeuIleAsnThrHsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
 Db 709 CAGAAGCTCAGCTGATCAACACCAACGCGAGTGGCACCTCAATAGACAGCGCCCTGAAC 768  
 QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTrpHisHisLysPheAsn 90  
 Db 769 TGCATGATAGCTCAACACCGGCTGTGTGGCAGGGCTTTTCTATCACCACAAAGTTCAAC 828  
 QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
 Db 829 TCTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCCAGCCCTTACCGATTTCACCAAGGC 888  
 QY 111 TrpGlyProIleSerTrpAlaAsnGlySerGlyProAspGlnArgProTrpHis 130  
 Db 889 TGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGACAGCGCCCTTACTGTGGCAC 948  
 QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
 Db 949 TACCCCCCAAACTTGGCGTATTGTGCCGCGAAGAGTGTGTGGTCCGGTATATTGC 1008  
 QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
 Db 1009 TTCACCTCCACGCCCCGTGTGTGGGAACGACGACAGGTGGCGCGCCACCTACAGC 1068  
 QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
 Db 1069 TGGGGTGAAATATACGACGCTTCCTGCTCTTAAACAATACAGGCGCCACCGTGGCAAT 1128  
 QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
 Db 1129 TGGTTCCGTTGTACCTGGATGAACCTCACTGGATTTCACCAAGTGTGGGAGCGCTCCT 1188  
 QY 211 CysValIleGlyAlaGlyAlaAsnThrLeuHisCysProThrAspCysPheArgLys 230  
 Db 1189 TGTGTATCGAGGGCGGCGCAACACACCCCTGCACCTGCCACCTGATTGCTTCCGCAAG 1248  
 QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 Db 1249 CATCCGGAGCCACATACCTCTCGGTGGGCTCCGGTCCCTGGATCACCCAGTGCCTG 1308  
 QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 Db 1309 GTCGACTACCGTATAGGCTTTGGCATTATCTTGTACCATCAACTACACTATATTTAA 1368  
 QY 271 IleArgMetTyrValGlyValGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
 Db 1369 ATCAGGATGTACGTGGAGGGTTCGAGCAGGCTGGAAGCTGCCTGCAACTGGACGG 1428  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 Db 1429 GCGCAACGTTCGATCTGGAAGATAGGGAGAGTCCGAG 1467  
 RESULT 6  
 AAT18246  
 ID AAT18246 standard; DNA; 1989 BP.  
 AC AAT18246;  
 XX  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 04-JUN-1996 (first entry)  
 XX  
 XX HCV1 E2/NS2 region DNA.  
 DE  
 XX HCV1; E1 protein; E2 protein; truncation; vaccine; diagnosis; therapy;  
 KW protein secretion; ds.  
 XX

OS Hepatitis C virus.  
 XX  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..63  
 FT mat\_peptide /\*tag= a  
 FT 64..1986 /\*tag= b  
 FT  
 XX  
 PN WO9604301-A2.  
 XX  
 PD 15-FEB-1996.  
 XX  
 XX 26-JUL-1995; 95WO-US010035.  
 XX  
 PR 29-JUL-1994; 94US-00282959.  
 PR 25-JUL-1995; 95US-00506608.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 XX Selby M, Houghton M;  
 XX  
 DR WPI; 1996-129331/13.  
 DR P-P8DB; AAR92935.  
 XX  
 PT Secretable hepatitis C virus E1 and E2 polypeptide(s) lacking all/part of  
 PT the membrane spanning domain - useful in vaccines, and for diagnostic and  
 PT therapeutic purposes, e.g. in assays for HCV.  
 XX  
 PS Disclosure; Fig 4a-4c; 46pp; English.  
 XX  
 CC The hepatitis c virus (HCV) E2/NS2 region (AAT18245) codes for the  
 CC envelope E2+NS2 proteins (AAR92935). Elimination of sequences encoding  
 CC the C-terminal membrane-spanning domain (approx. amino acids 337-361) of  
 CC E2 provides a truncated protein that can be secreted when produced  
 CC recombinantly in host cells. Truncated versions of the E1 protein (see  
 CC AAR92934) are similarly produced. When co-expressed or combined after  
 CC separate expression, the truncated E2 and E1 proteins form a complex. The  
 CC truncated proteins and complex are useful in vaccines and for diagnostic  
 CC and therapeutic apps. (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 1989 BP; 373 A; 586 C; 568 G; 462 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1,61e-110 Length: 1989  
 Score: 1620.50 Matches: 283  
 Percent Similarity: 96.93% Conservative: 1  
 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: Gaps: 1  
 US-10-715-665-7\_COPY\_1\_303 (1-303) x AAT18246 (1-1989)  
 QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
 Db 31 GTGCTGCTGCTATTTTCCGGCGTC-----GACGCGGAAACCCACGTCAC 75  
 QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
 Db 76 GGGGGAAGTCCGGCCACACTGTGTCTGGATTGTGTAGCTCTCGCACAGCGCCAA 135  
 QY 51 GlnAsnValGlnLeuIleAsnThrHsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
 Db 136 CAGAAGCTCAGCTGATCAACACCAACGCGAGTGGCACCTCAATAGACAGCGCCCTGAAC 195  
 QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTrpHisHisLysPheAsn 90  
 Db 196 TGCATGATAGCTCAACACCGGCTGTGTGGCAGGGCTTTTCTATCACCACAAAGTTCAAC 255  
 QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
 Db 256 TCTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCCAGCCCTTACCGATTTCACCAAGGC 315







DT 15-JAN-2001 (first entry)  
 XX cDNA sequence compiled Hepatitis C virus cDNA clones.  
 DE Hepatitis C virus; HCV; antiense polynucleotide; polyprotein;  
 KW viral infectivity; viral replication; ds.  
 KW Hepatitis C virus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 PH 1..8316  
 FT /\*tag= a  
 FT /note= "partial sequence; no termination codon given"  
 FT  
 XX  
 XX EP1034785-A2.  
 XX  
 XX 13-SEP-2000.  
 XX  
 XX 16-MAR-1990; 2000EP-00109602.  
 XX  
 XX 17-MAR-1989; 89US-00325338.  
 PR 20-APR-1989; 89US-00341334.  
 PR 18-MAY-1989; 89US-00355002.  
 PR 16-MAR-1990; 90EP-00302866.  
 XX  
 XX (CHIR ) CHIRON CORP.  
 PA  
 XX Houghton M, Choo Q, Kuo G;  
 PI  
 XX WPI; 2000-566891/53.  
 DR P-PSDB; AAB18540.  
 DR  
 XX  
 XX Novel composition comprising a hepatitis C virus antisense polynucleotide  
 PT which is complementary to or corresponds to a sense strand of the virus  
 PT genome, and selectively hybridizes to it.  
 XX  
 XX Example; Fig 16; 75pp; English.  
 PS  
 XX  
 XX The specification describes a pharmaceutical composition which comprises  
 CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is  
 CC characterized by a positive stranded RNA genome which has 40% homology at  
 CC the polypeptide level to a HCV polyprotein. The antisense polynucleotide  
 CC binds to cellular polynucleotides which enhance and/or are required for  
 CC viral infectivity, replicative ability or chronicity. The antisense  
 CC polynucleotides may also be designed to bind with high specificity, to be  
 CC of increased stability, to be stable and to have low toxicity. The  
 CC composition also comprises an agent which causes viral RNA to be  
 CC inactive. The composition is used for preventing HCV replication in a  
 CC system. The present sequence represents a novel HCV cDNA sequence, which  
 CC is used in the course of the invention  
 XX  
 SQ Sequence 8316 BP; 1671 A; 2529 C; 2345 G; 1771 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 8,76e-110 Length: 8316  
 Score: 1620.50 Matches: 283  
 Percent Similarity: 96.93% Conservative: 1  
 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: 3 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x AAA75296 (1-8316)  
 QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
 DB 778 GTGCTGCTGCTATTGCGCGGCTC-----GACCGGAAACCCACGTCACC 822  
 QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
 DB 823 GGGGGAAGTCCCGCCACACTGTGTGGATTGTGGCTCTCGCACCAGGCGCAG 882  
 QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70

DB 883 CAGAACGTCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCAGCGCCCTGAAC 942  
 QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90  
 DB 943 TGAATATGATAGCTCAACACCGGCTGGTGGAGGGCTTTTCTATATCAACCAAGTTCAAC 1002  
 QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
 DB 1003 TCTTCAGGCTGTCTGAGAGGCTAGCAGCTGCGACCCCTTACCGATTGTACAGGGC 1062  
 QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
 DB 1063 TGGGGCCCTATCATGTTATGCCAACGGAAGCGGCCCGACAGGCCCTACTTGTGGCAC 1122  
 QY 131 TyrProProlyserProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
 DB 1123 TACCCCCCAAAACCTTGGCGTATTGTGCCCGGAAAGAGTGTGTGGTGGTATATTGC 1182  
 QY 151 PheThrProSerProValValValGlyThrAspArgSerGlyAlaProThrTyrSer 170  
 DB 1183 TTCACCTCCACGCCCCGTGGTGGGAAACGACGACAGGTTCGGCGCGCCCTACAGC 1242  
 QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
 DB 1243 TGGGGTGAATAATGATACGGACGCTTTCGTCTCTTAACAATACACAGGCCCGCTGGGCAAT 1302  
 QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
 DB 1303 TGTTTCGGTGTGATACCTGGATGAACCTCACTGGGATTACCAAGTGTGGGAGCGCTCCT 1362  
 QY 211 CysValIleGlyAlaGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
 DB 1363 TGTGTCTATCGGAGGGCGGGCAACACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1422  
 QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 DB 1423 CATCCGAGCCACATACCTCTCGGTGGGCTCGGTCTCGGTCTCGGTCTCGGTCTCGGTCTG 1482  
 QY 251 ValAspTyrProTyrArgLeuTyrHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 DB 1483 GTGACTACCGGTATAGGCTTTGGCAATTATCTTGTACCATCACTACCATATTTAAA 1542  
 QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTyrThrArg 290  
 DB 1543 ATCAGATGTAGCTGGAGGGGTTCGAACACAGGCTGGAAGTCTGCTGCACTGCACTGCA 1602  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 DB 1603 GCGCAACGTTGGGATCTGGAAGACAGGACAGGACAGGTCGGAG 1641  
 RESULT 10  
 ADN35977  
 ID ADN35977 standard; cDNA; 8316 BP.  
 XX  
 XX AC ADN35977;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE HCV cDNA clone #1.  
 XX  
 KW Antiviral; Vaccine; hepatitis C virus infection; HCV infection; ss.  
 OS Hepatitis C virus.  
 XX  
 XX EP1394255-A2.  
 XX  
 PD 03-MAR-2004.  
 XX  
 XX 16-MAR-1990; 2003EP-00016585.  
 PF  
 XX 17-MAR-1989; 89US-00325338.  
 PR 20-APR-1989; 89US-00341334.  
 PR 18-MAY-1989; 89US-00355002.

PR 16-MAR-1990; 90EP-00302866.  
 XX (CHIR ) CHIRON CORP.  
 PA Houghton M, Choo Q, Kuo G;  
 XX WPI; 2004-193149/19.  
 DR P-PSDB; ADN35976.  
 XX Novel purified hepatitis C virus polypeptide comprising epitope encoded  
 PT by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C  
 PT virus.  
 XX Example 1; Fig 16; 79pp; English.  
 XX The present invention relates to hepatitis C virus (HCV) proteins and  
 CC cDNA sequences. The sequences are useful in immunoassays for detecting  
 CC antibodies directed against HCV antigen; preparing host cells transformed  
 CC with a recombinant polynucleotide; screening antiviral agents and  
 CC determining the effect of antiviral agent in inhibiting viral replication  
 CC in cell culture system; and developing vaccine for treating HCV  
 CC infection.  
 XX Sequence 8316 BP; 1671 A; 2537 C; 2338 G; 1770 T; 0 U; 0 Other;  
 SQ

Alignment Scores:  
 Pred. No.: 8.76e-110 Length: 8316  
 Score: 1620.50 Matches: 283  
 Percent Similarity: 96.93% Conservative: 1  
 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: 12 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x ADN35977 (1-8316)

QY 11 ValLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
 DB 778 GTGCTGCTGCTATTGCCGGGCTC-----GACGCGGAACCCACGTCACC 822

QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
 DB 823 GGGGGAAGTGGCGGCACACTGTGCTGGATTGTTAGCTCTCTGACACAGGCGCAAG 882

QY 51 GlnAsnValGlnLeuLeuLeuThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
 DB 883 CAGACGTCAGCTGATCAACACACGCGAGTGGCCTCAATAGCACGCGCCCTGAAC 942

QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyHisIleLysPheAsn 90  
 DB 943 TGCATATGATAGCTCAACACCGGCTGTTGGCAGGCTTTTCTATCACCACAGTTCAAC 1002

QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
 DB 1003 TCTTCAGGCTGTCTCAGAGGCTAGCCAGCTGCGGACCCCTTACCGATTTCACAGGCGC 1062

QY 111 TrpGlyProIleSerTrpAlaAsnGlySerGlyProAspGlnArgProTyCysTrpHis 130  
 DB 1063 TGGGGCCCTATCATGTTATGCCAACGGAAGCGGCGCCGACGAGCGCCCTACTGCTGGCAC 1122

QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyCys 150  
 DB 1123 TACCCCCCAAAACCTTGGCGGTATGTGCCCGGGAAGAGTGTGTGGTTCGGTATATTGC 1182

QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTySer 170  
 DB 1183 TTCACCTCCAGCCCGTGGTGGTGGGAACGACGACAGGTGCGGCGCGCCACCTACAGC 1242

QY 171 TrpGlyGlnAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
 DB 1243 TGGGGTGAATAATGATACGACGCTTCTCGTCTTAAACAATACCAAGGCGCCGCTGGGCAAT 1302

QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210

Db 1303 TGGTTCGGTTGTACTGATGAACCTCAACTGGATTACCAAGTGTGGGAGCGCTCT 1362  
 QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
 Db 1363 TGTGTCAATCGGAGGCGGCAACACACCTCTGCACTGCCCTGATTTGCTTCGCAAG 1422  
 QY 231 HisProAspAlaThrTySerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 Db 1423 CATCGGACGGCACATCTCTCGGTGCGGCTCCGCTCCGATCACACCCAGGTGCTG 1482  
 QY 251 ValAspTyProTyArgLeuTrpHisTyProCysThrIleAsnTyThrIlePheLys 270  
 Db 1483 GTCGACTACCCGTATAGGCTTTGGCATTTATCTCTGTACCATCACTACCATATTTAA 1542  
 QY 271 IleArgMetTyValGlyGlyValGluHisArgLeuGluAlaCysAsnTrpThrArg 290  
 Db 1543 ATCAGGATGTACGTGGAGGGTCCGACACAGGCTGGAAGCTGCTGCAACTGGACGGG 1602  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 Db 1603 GCGGAACGTTGCGATCTGGAACAGGACAGGTCGAG 1641

RESULT 11  
 AAQ05956  
 ID AAQ05956 standard; DNA; 9185 BP.  
 XX  
 AC AAQ05956;  
 XX 25-MAR-2003 (revised)  
 DT 23-JAN-1991 (first entry)  
 XX  
 DE Sense strand of the compiled Hepatitis C virus cDNA sequence.  
 XX  
 KW Hepatitis C virus (HCV); antiviral agent; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_RNA 1..1667  
 FT /tag= b  
 FT /note= "epitope within this region is claimed"  
 FT CDS 320..9185  
 FT /tag= a  
 FT misc\_RNA 8978..9185  
 FT /tag= c  
 FT /note= "encodes an epitope that is claimed"  
 XX  
 PN EP388232-A.  
 XX  
 PD 19-SEP-1990.  
 XX  
 PF 16-MAR-1990; 90EP-00302866.  
 XX  
 PR 17-MAR-1989; 89US-00325338.  
 PR 20-APR-1989; 89US-00341334.  
 PR 18-MAY-1989; 89US-00355002.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Houghton M, Choo QL, Kuo G;  
 XX  
 DR WPI: 1990-284418/38.  
 DR P-PSDB; AAR08124.  
 XX  
 PT Hepatitis C virus DNA - used for producing probes, polypeptide(s),  
 PT antibodies and anti-sense polynucleotide(s) for diagnosis and therapy.  
 XX  
 PS Disclosure; Fig 17; 83pp; English.  
 XX  
 CC HCV cDNA libraries were constructed using pooled serum from a chimpanzee  
 CC with chronic HCV infection. A lambda gIII library was screened with  
 CC probes derived from previously isolated clones. The ORF is derived from  
 CC the overlapping clones b114a, ag30a, CA205a, CA216a, p14a,

CC CA167b, CA156e, CA84a, CA59a, K9-1, 26j, 13i, 12f, 14i, 11b, 7f, 8h, 33c, 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g, 39c, 35f, 19g, 26g, 15e, b5a and 16jh. These clones extend the sequence of the HCV genome reported in EP-318216. The upstream region from nucleotides -319 to +1348 (-1-1667 in this file) is covered by clones b114a, 18g, ag30a, CA205a, CA290a, CA216a, p14a, CA167b, CA156e, CA84a and CA59a; nucleotides 8659-8866 (-8978-9185 in this file) are covered by clones b5a and 16jh. See also AAQ05955. (Updated on 25-MAR-2003 to correct PA field.)

SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 9,86e-110 Length: 9185  
Score: 1620.50 Matches: 283  
Percent Similarity: 96.93% Conservative: 1  
Best Local Similarity: 96.59% Mismatches: 4  
Query Match: 92.81% Indels: 5  
DB: 2 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x AAQ05956 (1-9185)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
DB 1439 GTGCTGCTGCTATTGGCGGCGTC-----GACGCGAAACCCACGTCACC 1483  
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
DB 1484 GGGGGAAGTCCCGCCACACTGTGCTGTGGATTGTTAGCTCTCCGACAGGCGCAAG 1543  
QY 51 GlnAsnValGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 70  
DB 1544 CAGAACGTCAGCTGATCAACACACGCGAGTTGGCACCTCAATAGCAGGCGCTGAAC 1603  
QY 71 CysAsnAspSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 90  
DB 1604 TGCATGATAGCTCAACACCGGCTGGTGGAGGGCTTTTCTATCACCAAGTTCAAC 1663  
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
DB 1664 TCTTACGCTGCTCTGAGAGCTAGCCAGCTGCCAGCCCTTACCGATTGACAGGCG 1723  
QY 111 TrpGlyProLeuSerTyrrAlaAsnGlySerGlyProAspGlnArgProTyrrCysTrpHis 130  
DB 1724 TGGGGCCCTATCATGTTATGCAACGGAAGCGGCGCCACAGCGCGCCCTACTGCTGCGAC 1783  
QY 131 TyrProProLysProCysGlyIleValProAlaIysSerValCysGlyProValTyrrCys 150  
DB 1784 TACCCCAAAACCTTTCGGGTATTGTCGCCCGGAAGAGTGTGTGTCGGGTATATTGC 1843  
QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrrSer 170  
DB 1844 TTCACCTCCAGCCCGTGGTGGTGGNACGACCGACAGGTTCGGCGGCCACCTACAGC 1903  
QY 171 TrpGlyGlnAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
DB 1904 TGGGGTGAAATGATACGAGCGCTTTCGCTCTTAAACAATACACGCGCCACCGCTGGCAAT 1963  
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
DB 1964 TGGTTCGGTGTACCTGGATGAACCTCAACTGGATTTCACCAAGTGTGCGAGGCGCTCCT 2023  
QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
DB 2024 TGTGTCATCGAGGGGGGCGACACACCTTCGACTGCTGCCCTGCTGCTTCCGCAAG 2083  
QY 231 HisProAspAlaThrTyrrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
DB 2084 CATCCGAGCCACATACTCTCGGTGCGGCTCCGGTCCCTGGATTCACACCGAGTGCCTG 2143  
QY 251 ValAspTyrrProTyrrArgLeuTrpHisTyrrProCysThrIleAsnTyrrIlePheLys 270  
DB 2144 GTGACTTACCCGTATAGGCTTTGGCAATTATCTTGTACCATCAACTACACCATATTATAA 2203

QY 271 IleArgMetTyrrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
DB 2204 ATCAGGATGTACGTGGAGGGGTGGAACAGAGCTGGAAGCTGCTGCAACTGGACCGG 2263  
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
DB 2264 GGGCAACGTTGCGATCTGGAAGACAGGACAGGAGGTCCGAG 2302  
RESULT 12  
AAQ10566  
ID AAQ10566 standard; DNA; 9185 BP.  
XX AC  
XX AAQ10566;  
XX AC  
DT 25-MAR-2003 (revised)  
DT 29-APR-1991 (first entry)  
XX DT  
XX DE Hepatitis C virus strain 1 DNA.  
XX KW Hepatitis C virus; HCV-1; non-A, non-B hepatitis; HCV antigen;  
XX KW viral infections; ss.  
XX OS Hepatitis C virus.  
XX PN EP414475-A.  
XX PD 27-FEB-1991.  
XX PF 21-AUG-1990; 90BP-00309120.  
XX PR 25-AUG-1989; 89US-00398667.  
XX PA (CHIR ) CHIRON CORP.  
XX PI Weiner AJ, Steimer KS;  
XX WPI; 1991-059670/09.  
XX Cell lines infected with hepatitis C virus - are used as source of  
XX PT antigens for detection of HCV antibodies, for vaccines, and for screening  
XX anti-viral agents.  
XX PS Disclosure; Fig 1; 24pp; English.  
XX CC This is a hepatitis C virus (HCV) composite cDNA sequence, deduced using  
XX CC overlapping clones. a compsn. contg. the antigenic protein encoded by  
XX CC this sequence is useful for detecting anti-HCV anti- bodies (Abs) and for  
XX CC screening an agent which inhibits HCV replic- ation. A cell line infected  
XX CC with this virus can be used as a source of antigens. The antigen is  
XX CC useful for preparing vaccines for treating viral infections. See also  
XX CC AAQ10567. (Updated on 25-MAR-2003 to correct PA field.)  
XX SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 9,86e-110 Length: 9185  
Score: 1620.50 Matches: 283  
Percent Similarity: 96.93% Conservative: 1  
Best Local Similarity: 96.59% Mismatches: 4  
Query Match: 92.81% Indels: 5  
DB: 2 Gaps: 1  
US-10-715-665-7\_COPY\_1\_303 (1-303) x AAQ10566 (1-9185)  
QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
DB 1439 GTGCTGCTGCTATTGGCGGCGTC-----GACGCGAAACCCACGTCACC 1483  
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
DB 1484 GGGGGAAGTCCCGCCACACTGTGCTGTGGATTGTTAGCTCTCCGACAGGCGCAAG 1543  
QY 51 GlnAsnValGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 70

```
Db      1544 CAGAACGTCAGCTGATCAACACCAACGCGAGTTGGCAGCTCAATAGACGCGCTTGAC 1603
Qy      71  CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyRHisHisLysPheAsn 90
Db      1604 TGCATATGATAGCTCAACACCGCTGGTTGGCAGGCTTTTCTATCACCACCAAGTTCAAC 1663
Qy      91  SerSerGlyCyProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db      1664 TCTTCAGGCTGTCCTGAGAGGTAGCCAGCTCGCAGCCCTTACCAGATTTTACCAGGCG 1723
Qy      111 TrpGlyProIleSerTyRAlaAsnGlySerGlyProAspGlnArgProTyRHis 130
Db      1724 TGGGGCCCTATCAGTTATGCCAAGGAGCGGCCCGACCGCCCTTACTGTGGCAC 1783
Qy      131 TyRProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyR 150
Db      1784 TACCCCCCAAAACCTTGGCGTATTTGGCCGCGAAGAGTGTGTGGTCCGGTATATTGC 1843
Qy      151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyR 170
Db      1844 TTCACTCCAGGCCCTGTGTGGTGGGAACGACGACGAGTCGGCGCGCCCACTTACAGC 1903
Qy      171 TrpGlyGluAsnAspThrAspValPheValLeuAsnThrArgProProLeuGlyAsn 190
Db      1904 TGGGGTGAATAATGATACGAGCTCTTCGTCTTAACATACAGGCCACCGCTGGCAAT 1963
Qy      191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaPro 210
Db      1964 TGTTCCGTTGTACCTGGATGAATCACTGGATTCAACAAAGTGTGGAGCGGCTCCT 2023
Qy      211 CysValIleGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db      2024 TGTGTATCGAGGGCGCGGCAACACACCTGCACCTGCCACCTGATGCTTCCGCAAG 2083
Qy      231 HisProAspAlaThrTyRSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db      2084 CATCCGAGCCACATACTCTCGGTGGGCTCCGGTCCCTGGATCATACCCAGGTGCTG 2143
Qy      251 ValAspTyRProTyRArgLeuTrpHisTyRProCysThrIleAsnTyRThrIlePheLys 270
Db      2144 GTCGACTACCGGTATAGGCTTTGGCATTTATCTGTGTACCATCAACTACACCATATTTAA 2203
Qy      271 IleArgMetTyRValGlyValGluHisArgLeuGluAlaAlaCysAsnThrThrArg 290
Db      2204 ATCAGGATGTACGTGGAGGGGTGGAACACAGCTGGAAGCTGCTGCAACTGGACGG 2263
Qy      291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db      2264 GCGAACGTTGCGATCTGGAAGACAGGACAGGATCCGAG 2302

RESULT 13
ID AAX00459
XX AAX00459 standard; DNA; 9185 BP.
XX AAX00459;
XX AAX00459;
DT 10-MAY-1999 (first entry)
XX
DE Hepatitis C virus 1 ORF1.
XX
KW HCV; non-A, non-B hepatitis; NANBH; diagnosis; vaccine; antigen;
KW antibody; immunoassay; assay; ss.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT CDS 320..9185
FT /tag= a
XX
PN US5856437-A.
XX
XX 05-JAN-1999.
```

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XX      03-NOV-1994; 94US-00334255.
PF
XX      15-SEP-1989; 89US-00408045.
PR      21-DEC-1989; 89US-00456142.
PR      04-JAN-1991; 91US-00637380.
PR      02-AUG-1993; 93US-00101280.
PR      24-FEB-1994; 94US-00201066.
XX
XX (NAHE-) NAT INST OF HEALTH JAPAN.
PA (CHIR ) CHIRON CORP.
XX
XX Weiner AJ, Miyamura T, Irvine BD, Kolberg JA, Han J, Saito I;
PI Cha T, Houghton M;
XX
XX WPI; 1999-105191/09.
XX
XX Antigenic polypeptides from J1 and J7 hepatitis C virus isolates - useful
PT as immunoassay reagents, for raising antibodies and as vaccine
PT components.
XX
XX Disclosure; Fig 12A-C; 44pp; English.
XX
XX This is the nucleotide sequence of ORF1 of hepatitis C virus prototype
CC HCV-1. The invention relates to 2 new isolates, J1 and J7, of HCV. These
CC new isolates comprise nucleotide (see AAX00400-04) and amino acid (see
CC AAW30583-87) sequences which are distinct from HCV1. Thus J1 and J7
CC provide new polynucleotides and polypeptides useful in diagnostics,
CC recombinant protein production and vaccine development. Claimed
CC polypeptides can be used: (i) as immunoassay reagents, or standards, to
CC detect HCV antibodies, e.g. for diagnosing infection or screening donated
CC blood; (ii) to generate specific antibodies (used for detecting the
CC corresponding polypeptide, to screen for antiviral agents, for virus
CC isolation and for passive immunisation); (iii) in protective or
CC therapeutic vaccines, and (iv) for isolation of non-A, non-B viruses
XX
XX Sequence 9185 BP; 1849 A; 2793 C; 2605 G; 1938 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 9,86e-110 Length: 9185
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 2 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x AAX00459 (1-9185)
Qy      11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db      1439 GTGCTGCTGCTATTTCGCGGCTC-----GACGCGGAAACCCACGTCACC 1483
Qy      31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db      1484 GGGGGAAGTGGCGGCCACACTGTGTGATTGTTAGCTCTCTCGCACGCGCGCAAG 1543
Qy      51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db      1544 CAGAACGTCAGCTATCAACACCAACGCGAGTGGCAGCTTCAATAGACGCGCCCTGAAAC 1603
Qy      71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyRHisHisLysPheAsn 90
Db      1604 TGCATATGATAGCTCAACACCGCTGGTTGGCAGGCTTTTCTATCACCACCAAGTTCAAC 1663
Qy      91 SerSerGlyCyProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db      1664 TCTTCAGGCTGTCCTGAGAGGTAGCCAGCTCGCAGCCCTTACCAGATTTTACCAGGCG 1723
Qy      111 TrpGlyProIleSerTyRAlaAsnGlySerGlyProAspGlnArgProTyRHis 130
Db      1724 TGGGGCCCTATCAGTTATGCCAAGGAGCGGCCCGACCGCCCTTACTGTGGCAC 1783
Qy      131 TyRProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyR 150
```

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Db 1784 TACCCCAACACCTTCGGGTATTTGTCGCCGGAAGAGTGTGTGTGGTGGTATATTC 1843
Qy 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 1844 TTCACCTCCAGCCCCGTTGGTGGGAAACGACAGGTGGGGCGGCCACCTACAGC 1903
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1904 TGGGGTCAAAATGATACGGAGCTCTCGTCTTAACAATACACGCGCCACGCTGGGCAAT 1963
Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 1964 TGGTTCGGTGTACCTCGGATGAACCTCAACTGGATTCCACAAAGTGTGCGAGCGCTTCCT 2023
Qy 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 2024 TGTGTCTATCGAGGGGGGGGCAACACACCTCGACCTGCCCTCACTGATTCCTCCGCAAG 2083
Qy 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 2084 CATCCGAGCGCACATACCTCGGTGGGGCTCCGCTCCCTGGATCACACCCAGGTGCGCTG 2143
Qy 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 2144 GTCGACTACCCGCTATAGGCTTTTGGCAATTATCTTGTATCACTCAACTACACCATATTTAA 2203
Qy 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
Db 2204 ATCAGGATGTACGTGGAGGGGTGCAACAGGCTGGAAGTGGCTGCTGCAACTGACGCGG 2263
Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 2264 GCGCAACGTTGCGATCTGGAAGACAGGACAGGTCGCGAG 2302

RESULT 14
AAZ26737
ID AAZ26737 standard; DNA; 9185 BP.
XX
AC AAZ26737;
XX
DT 21-JUN-1999 (first entry)
XX
DE Nucleotide sequence of the ORF of HCV1.
XX
KW HCV; J7 isolate; J1 isolate; HCV1; immunoassay; asiatic strain;
KW diagnosis; HCV infection; blood screening; immunisation; antiviral; ss.
XX
OS Hepatitis C virus.
XX
PN US5871903-A.
XX
PD 16-FEB-1999.
XX
PF 08-MAY-1995; 95US-00436965.
XX
PR 15-SEP-1989; 89US-00408045.
PR 21-DEC-1989; 89US-00456142.
PR 04-JAN-1991; 91US-00637380.
PR 02-AUG-1993; 93US-00101280.
PR 24-FEB-1994; 94US-00201066.
PR 03-NOV-1994; 94US-00334255.
XX
(NAHE-) NAT INST OF HEALTH JAPAN.
PA (CHIR ) CHIRON CORP.
XX
PI Saito I, Miyamura T;
XX
WIPI; 1999-166619/14.
XX
DR Immunoassays for Asiatic strains of hepatitis C virus - for diagnosis of
PT infection and screening blood supplies.
XX
```

PS Disclosure; Fig 12A-C; 43pp; English.

XX The present sequence represents the sequence of ORF1 of hepatitis C virus (HCV) isolate HCV1. The specification describes new isolates of HCV, J1 and J7. J1 and J7 isolates comprise sequences which are distinct from the prototype HCV isolates, HCV1. The specification describes immunoassays for HCV based on antigens from Asiatic strains not cross-reactive with HCV-1. The assays are used for diagnosis of HCV infection and to screen donated blood. The anti-HCV antibodies are also useful therapeutically and prophylactically (passive immunisation); in screening for antiviral agents; for isolation, purification and identification of non-A, non-B hepatitis virus (e.g. by affinity chromatography) and to raise anti-idiotypic antibodies (useful for treatment or diagnosis and to determine immunogenic regions of the HCV antigens)

XX SQ Sequence 9185 BP; 1849 A; 2792 C; 2606 G; 1938 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 9,86e-110 Length: 9185  
Score: 1620.50 Matches: 283  
Percent Similarity: 96.93% Conservatives: 1  
Best Local Similarity: 96.59% Mismatches: 4  
Query Match: 92.81% Indels: 5  
DB: 2 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x AAZ26737 (1-9185)

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Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 1439 GTGCTGCTGCTATTTGTCGGCGCTC-----GACGGGAAACCCACGTCAAC 1483
Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 1484 GGGGGAAGTCCCGCCACACTGTGTCTGGATTGTTAGCTCTTCGCACAGCGGCCAG 1543
Qy 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 1544 CAGAACGTCAGCTGATCAACACACGCGCAGTTGGCACCCTCAATAGCAGCGCCCTGAC 1603
Qy 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90
Db 1604 TGCAATGATAGCTCAACACCGGCTGGTTGGAGGGCTTTTCTATCACCACAGTTCAAC 1663
Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1664 TCTTCAGGCTGCTCCTCAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTGACCGAGG 1723
Qy 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 1724 TGGGGCCCTATCAGTTATGCCAACGGAAGCGGCGCCCGACCGAGCGCCCTACTGCTGGC 1783
Qy 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 1784 TACCCCCCAAAACCTTTCGGGTATTTGCCCCGGAAGAGTGTGTGTCCGGTATATTC 1843
Qy 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 1844 TTCACCTCCAGCCCCGTTGGTGGGAAACGACGAGGTGGGGCGGCCACCTACAGC 1903
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1904 TGGGGTGAATAATGATACGGACGCTTTCGCTCTTAAACAATACACGAGCGCCCTGGGCAAT 1963
Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 1964 TGGTTCGGTGTACCTCGGATGAACCTCAACTGGATTCCACAAAGTGTGCGAGCGCTTCCT 2023
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Db 2024 TGTGTCTATCGAGGGGGGGGCAACACACCTGCACTGCCCTCACTGATTCCTCCGCAAG 2083
Qy 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
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Db 2084 CATCCGAGCCACATACCTCTCGGTCCGGCTCCGGTCCCTGGATCACACCCAGTGCCTG 2143  
 QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 Db 2144 GTGACACTACCCGTATAGGCTTTGGCATATCTCTGTACCATCAACTACACCATATTTAAA 2203  
 QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
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 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 Db 2264 GCGGAACGTTGGATCTGGAACACAGGACAGTCCGAG 2302

RESULT 15  
 ADF66068  
 ID ADF66068 standard; DNA; 9185 BP.  
 XX AC ADF66068;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Hepatitis C virus 1 ORF nucleotide sequence.  
 XX  
 KW Hepatitis C virus; HCV; screening; identification; non A non B hepatitis;  
 KW NANBH; gene; ds.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN US5959092-A.  
 XX  
 PD 28-SEP-1999.  
 XX  
 PF 08-MAY-1995; 95US-00436966.  
 XX  
 PR 15-SEP-1989; 89US-00408045.  
 PR 21-DEC-1989; 89US-00456142.  
 PR 04-JAN-1991; 91US-00637380.  
 PR 02-AUG-1993; 93US-00101280.  
 PR 24-FEB-1994; 94US-00201066.  
 PR 03-NOV-1994; 94US-00334255.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (NAHE-) NAT INST OF HEALTH JAPAN.  
 XX  
 PI Saito I, Miyamura T;  
 XX  
 XX WPI; 1999-570774/48.  
 XX  
 PT Polynucleotide probes useful for screening and identifying carriers of  
 PT non A non B hepatitis.  
 XX  
 PS Disclosure; Fig 12; 44pp; English.  
 XX  
 CC The present invention describes polynucleotides sequences from Hepatitis  
 CC C virus (HCV) isolates J7 C/E, J1 E, J1 E/NS1, J1 NS3, and J1 NS5 or from  
 CC deposits BP-2593, BP2594, BP-2637 and BP-2638. The  
 CC polynucleotide sequences are useful as probes for screening and  
 CC identifying carriers of non A non B hepatitis (NANBH). The present  
 CC sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 9185 BP; 1849 A; 2792 C; 2606 G; 1938 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 9,86e-110 Length: 9185  
 Score: 1620.50 Matches: 283  
 Percent Similarity: 96.93% Conservative: 1  
 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: 2 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x ADF66068 (1-9185)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
 Db 1439 GTGCTGCTGCTATTTTGGCCGGGCTC-----GAGCGGGAACCCACGTCACCC 1483  
 QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
 Db 1484 GGGGGAAGTGGCGGCCACACTGTGTCTGATTTGTAGCTCTCTCGACCGCCCAAG 1543  
 QY 51 GlnAenValGlnLeuIleAenThrAsnGlySerTrpHisLeuAenSerThrAlaLeuAen 70  
 Db 1544 CAGAACGTCAGCTCATCAACACCAACCGCAGTTGGCACCTCAATAGCACGGCCCTGAAC 1603  
 QY 71 CysAsnAspSerLeuAsnThrClyTrpLeuAlaGlyLeuPheTyrHisIleLysPheAen 90  
 Db 1604 TGCAATGATAGCCTCAACACCGGCTGGTTGGCAGGGCTTTCTATCACCACAAAGTTCAAC 1663  
 QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
 Db 1664 TCTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACCCAGGCG 1723  
 QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
 Db 1724 TGGGGCCCTATCAGTTATGCCAACCGAAGCGGCCCGACCGGCCCTTACTGTGTCGAC 1783  
 QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
 Db 1784 TACCCCCCAAAACCTTGGCGGTATTGTGCCCGGAAGAGTGTGTGGTTCGGTATATTGC 1843  
 QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
 Db 1844 TTCACCTCCCGCCCGTGGTGGGAACGACCGACAGTGGCGCGGCCACCTACACG 1903  
 QY 171 TrpGlyGluAenAspThrAspValPheValLeuAenAsnThrArgProProLeuGlyAen 190  
 Db 1904 TGGGGTGAATAATGATACGACGCTCTTCGTCTTAAACATACCAGGCCACCGCTGGGCAAT 1963  
 QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
 Db 1964 TGGTTCGGTGTGTACCTGGATGAACCTCAACTGGATTTCACCAAGTGTGGAGCGGCTCCT 2023  
 QY 211 CysValIleGlyGlyAlaGlyAsnThrLeuHisCysProThrAspCysPheArgLys 230  
 Db 2024 TGTGTATCGAGGGCGGGCAACACACCTGCTGCACTGCCCTGCTGCTTCCGCAAG 2083  
 QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 Db 2084 CATCCGAGCCACATACCTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTGCTG 2143  
 QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 Db 2144 GTGACTACCCGTATAGGCTTTGGCATATTCCTTGTACCATCACTACACCATATTTAAA 2203  
 QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
 Db 2204 ATCAGGATGTACGTGGAGGGGTGGAACACAGGCTGGAAGCTGCTGCAACTGGACCGCG 2263  
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 Db 2264 GCGGAACGTTGGATCTGGAACACAGGACAGGACAGTCCGAG 2302

Search completed: April 15, 2005, 06:42:44  
 Job time : 633 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 15, 2005, 04:52:33 ; Search time 202 Seconds  
(without alignments)

2454.415 Million cell updates/sec

Title: US-10-715-665-7\_COPY\_1\_303

Perfect score: 1746

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1620.5	92.8	1207	1	US-08-325-630-12
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9	1620.5	92.8	1989	3	US-09-415-582-4
10	1620.5	92.8	1989	4	US-09-693-596-3
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12	1620.5	92.8	8987	3	US-08-444-818-137

13	1620.5	92.8	9185	3	US-08-444-818-122	Sequence 122, Appl
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15	1620.5	92.8	9379	3	US-09-388-874-1	Sequence 1, Appli
16	1620.5	92.8	9379	4	US-09-916-359-1	Sequence 1, Appli
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21	1615.5	92.5	9379	3	US-08-444-818-176	Sequence 176, App
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23	1526	87.4	5125	1	US-08-453-552-11	Sequence 11, Appl
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25	1526	87.4	5125	5	PCT-US93-00907-11	Sequence 11, Appl
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30	1521.5	87.1	9416	3	US-08-811-566-19	Sequence 19, Appl
31	1521.5	87.1	9416	3	US-09-034-756-19	Sequence 19, Appl
32	1518.5	87.0	9365	4	US-09-827-688-7	Sequence 7, Appli
33	1515.5	86.8	9646	3	US-08-811-566-1	Sequence 1, Appli
34	1515.5	86.8	9646	3	US-09-034-756-1	Sequence 1, Appli
35	1515.5	86.8	12980	3	US-08-811-566-5	Sequence 5, Appli
36	1515.5	86.8	12980	3	US-09-034-756-5	Sequence 5, Appli
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38	1514	86.7	7106	2	US-08-453-552-5	Sequence 5, Appli
39	1514	86.7	7106	2	US-08-710-637-5	Sequence 5, Appli
40	1514	86.7	7106	5	PCT-US93-00907-5	Sequence 5, Appli
41	1514	86.7	7106	5	PCT-US94-07280-8	Sequence 8, Appli
42	1514	86.7	7106	5	PCT-US95-01087-8	Sequence 8, Appli
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44	1514	86.7	7298	2	US-08-710-637-3	Sequence 3, Appli
45	1514	86.7	7298	5	PCT-US93-00907-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-721-480-6  
; Sequence 6, Application US/09721480  
; Patent No. 6740323  
; GENERAL INFORMATION:  
; APPLICANT: Selby, Mark  
; APPLICANT: Glazer, Edward  
; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE  
; FILE REFERENCE: PP01635.002  
; CURRENT APPLICATION NUMBER: US/09/721,480  
; CURRENT FILING DATE: 2000-11-22  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 5882  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: plasmid  
; OTHER INFORMATION: PCMV-II-E2661-sag  
; NAME/KEY: CDS  
; LOCATION: (1992)..(3584)  
US-09-721-480-6

Alignment Scores:  
Pred. No.: 1.07e-153 Length: 5882  
Score: 1746.00 Matches: 303  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-715-665-7\_COPY\_1\_303 (1-303) x US-09-721-480-6 (1-5882)

Qy 1 MetAspAlaMetIysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal 20

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Db      2112 TTGTGTAGCTCTCTGCACACGCGCCAAAGCAGAGCTCCAGCTGATCAACACCAACGCG 2171
QY      61  SerTrpHisLeuAenSerThrAlaLeuAenCysAenAspSerLeuAenThrGlyTrpLeu 80
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QY      101 CysArgProLeuThrAspPheAspGlnGlyTrpGlyProIleSerTyrAlaAenGlySer 120
Db      2292 TCCCGACCCCTTACCGATTTTGACACAGGCTGGGGCCCTATCAGTTATGCCAACCGAAGC 2351
QY      121 GlyProAspGlnArgProTyrCysTrpHisTyrProProLeuProCysGlyIleValPro 140
Db      2352 GGGCCCGACAGCGCCCTACTGTGGGCACTACCCCCCAAAACCTTGGGTATTTGGCCC 2411
QY      141 AlaLysSerValCysGlyProValTyrCysPheThrProSerProValValGlyThr 160
Db      2412 GCGAAGAGTGTGTGTCGGTATATTCCTTCACTCCACGCCCGTGGTGGGAACG 2471
QY      161 ThrAspArgSerGlyAlaProThrTyrSerTrpGlyGluAenAspThrAspValPheVal 180
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QY      181 LeuAenAsnThrArgProProLeuGlyAsnTrpPheGlyCysThrTrpMetAenSerThr 200
Db      2532 CTTAACAAATACCAAGGCCACCGCTGGGCAATTTGTCGGTTGACCTGGATGAACCTCACT 2591
QY      201 GlyPheThrLysValCysGlyAlaProProCysValIleGlyAlaGlyAenAenThr 220
Db      2592 GGATTCACCAAGTGTGGAGCGCTCTCTGTGTCTATCGAGGGCGGGCAACACACC 2651
QY      221 LeuHisCysProThrAspCysPheArgLysHisProAspAlaThrTyrSerArgCysGly 240
Db      2652 CTGCACTGCCCACTGATTCCTCCCAAGCATCCGGACGCCACATACCTCTCGGTGCGGC 2711
QY      241 SerGlyProTrpIleThrProArgCysLeuValAspTyrProTyrArgLeuTrpHisTyr 260
Db      2712 TCCGTCCTCTGGATCACCCAGGTCCTGTCGACTACCGTATAGGCTTTGGCATTAAT 2771
QY      261 ProCysThrIleAenTyrThrIlePheLysIleArgMetTyrValGlyGlyValGluHis 280
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QY      281 ArgLeuGluAlaAlaCysAenTrpThrArgGlyGluArgCysAspLeuGluAspArgAsp 300
Db      2832 AGGCTGGAAGCTCCCTGCAACTGGACGGGGGGAACGTTGGCATCTGGAAGATAGGAC 2891
QY      301 ArgSerGlu 303
Db      2892 AGGTCCGAG 2900

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RESULT 2

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US-08-460-806-12
; Sequence 12, Application US/08460806
; Patent No. 5747241
; GENERAL INFORMATION:
; APPLICANT: MIYAMURA, TATSUO
; APPLICANT: SAITO, IZUMU
; APPLICANT: HARADA, SHIZUKO
; APPLICANT: HONDA, YOSHIKAZU
; TITLE OF INVENTION: DIAGNOSTIC REAGENT FOR HEPATITIS C

```

```

; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,806
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,630
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: US 07/956,993
; FILING DATE: 06-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5747241man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4667-001-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis C virus
; IMMEDIATE SOURCE:
; CLONE: HCV1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1207
; US-08-460-806-12

```

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Alignment Scores:
Pred. No.: 6,63e-143 Length: 1207
Score: 1620.50 Matches: 283
Percent Similarity: 96.9% Conservative: 1
Best Local Similarity: 96.5% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 1 Gaps: 1

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US-10-715-665-7\_COPY\_1\_303 (1-303) x US-08-460-806-12 (1-1207)

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QY      11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db      104 GTGCTGCTGCTATTTGCCGCGTC-----GACGCGGAACCCACGTCACC 148
QY      31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db      149 GGGGGAAGTCCGGCCACACTGTGTGATTGTGTAGCTCTCGCACAGCGCCAAG 208
QY      51 GlnAenValGlnLeuIleAenThrAenGlySerTrpHisLeuAenSerThrAlaLeuAen 70
Db      209 CAGACGCTCCAGCTGATCAACACCAACGCGCAGTTGGCACTCAATAGCACGCGCTGAAC 268
QY      71 CysAenAspSerLeuAenThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAen 90
Db      269 TGCATATGATAGCTCAACACCGCGCTGGTGGCAGGGCTTTTCTATCACCACCAAGTTCAAC 328

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Qy 91 SerSerGlyCysProGluuArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 329 TCITCAGCGTCTCTGAGAGCTAGCAGCTGCCGACCCCTTACCGATTTCAGCAGGC 388
Qy 111 TrpGlyProIleSerTyAlaAenGlySerGlyProAspGlnArgProTyCysTrpHis 130
Db 389 TGGGGCCCTATCAGTTATGCAACGGAAGGGCCCGCCAGCAGGCCCTACTGTCGCAC 448
Qy 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 449 TACCCCAAAACCTTCGGTATTGTCGCCGGAAGAGTGTGTGTCGGTATATTGC 508
Qy 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 509 TTCACCTCCAGCCCGTGGTGGGAACGACGACAGGTGGCGCGCCCACTACAGC 568
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 569 TGGGGTGAATAATGATACGAGCTCTTCGTCCTTAACAATAACAGCCAGCCGCTGGGCAAT 628
Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 629 TGGTTCGGTTGACCTGGATGAACCTCAACTGGATTCCAAAGTGTGGGAGCGCTCCT 688
Qy 211 CysValIleGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 689 TGTGTCATCGAGGGGGGGCAACACACCTGCACCTGCCCTGATTCCTCCGCAAG 748
Qy 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 749 CATCCGAGCCACATACCTCGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 808
Qy 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 809 GTGACATACCGGTATAGGCTTTGGCATTTCTTGTACCACTCACTACCACTATTATAA 868
Qy 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
Db 869 ATCAGGATGATCGTGGGAGGGTGGAGACAGAGCTGGAGCTGCTGCACTGGAGCGG 928
Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 929 GGGCAACGTTGCGATCTGGAAGACAGGACAGGTCCGAG 967

```

RESULT 3

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US-08-325-630-12
; Sequence 12, Application US/08325630
; Patent No. 5750331
; GENERAL INFORMATION:
; APPLICANT: MIYAMURA, TATSUO
; APPLICANT: SAITO, IZUMU
; APPLICANT: HARADA, SHIZUKO
; APPLICANT: HONDA, YOSHIKAZU
; TITLE OF INVENTION: DIAGNOSTIC REAGENT FOR HEPATITIS C
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,630
; FILING DATE:
; CLASSIFICATION: 435

```

PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 07/956,993
; FILING DATE: 06-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5750331man P.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 4667-001-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1207 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis C virus
; IMMEDIATE SOURCE:
; CLONE: HCV1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..1207
; US-08-325-630-12

```

Alignment Scores:

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Pred. No.: 6,63e-143 Length: 1207
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 1 Gaps: 1

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US-10-715-665-7\_COPY\_1\_303 (1-303) x US-08-325-630-12 (1-1207)

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Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 104 GTGCTGCTGCTATTTCGCCGGCTC-----GACGGGANAACCCACGTCAAC 148
Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 149 GGGGGAAGTCCGGCCACACTGTGTCTGGATTGTTAGCTCTCTCGCACCAGCGCCAA 208
Qy 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 209 CAGAACGTCAGCTGATCAACACCAACGCGAGTGGCAGCTCAATAGCAGCGGCCCTGAAC 268
Qy 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisLysPheAsn 90
Db 269 TGCATGATGATGCTCAACACCGGCTGTTGGCAGGGCTTTCTATCACCACAGTTCAAC 328
Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 329 TCTTCAGGCTGCTCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTCAGCAGGC 388
Qy 111 TrpGlyProIleSerTyAlaAenGlySerGlyProAspGlnArgProTyCysTrpHis 130
Db 389 TGGGGCCCTATCAGTTATGCAACGGAAGGGCCCGCCAGCAGGCCCTACTGTCGCAC 448
Qy 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 449 TACCCCAAAACCTTCGGTATTGTCGCCGGAAGAGTGTGTGTCGGTATATTGC 508
Qy 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 509 TTCACCTCCAGCCCGTGGTGGGAACGACGACAGGTGGCGCGCCCACTACAGC 568
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 569 TGGGGTGAATAATGATACGAGCTCTTCGTCCTTAACAATAACAGCCAGCCGCTGGGCAAT 628

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Qy	191	TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaIaPro	210
Db	629	TGGTTCCGGTTGTACTCGATGAACACTCAACTGGATTCCACAAAGTGTGCGGAGCGCTCCT	688
Qy	211	CysValIleGlyGlyAlaGlyAsnThrLeuHisCysProThrAspCysPheArgLys	230
Db	689	TGTGTATCGAGGGGGGGCAACAACCCCTGCACTGCCCACTGATTGCTTCCGCAAG	748
Qy	231	HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu	250
Db	749	CATCCGGACGCCACATACTCTCGTGGCGGCTCCGGTCCCTGGATCACCCAGGTCGCTG	808
Qy	251	ValAspTyrProTyrArgLeuTriphHisTyrProCysThrIleAsnTyrThrIlePheLys	270
Db	809	GTCGACTACCCGTATAGCTTTGGCATTTATCCTTGTCACCATCACTACACCATATTTAAA	868
Qy	271	IleArgMetTyrValGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg	290
Db	869	ATCAGGATGTACGTGGGAGGGGTGAAACACAGCTGGGAAGCTGCCTGCAACTGGACGGG	928
Qy	291	GlyGluArgCysAspLeuGluAspArgAspArgSerGlu	303
Db	929	GGCCAAAGCTTCCGATCTCGAAGACAGGACAGCTCCGAG	967

## RESULT 4

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US-08-483-695-35
: Sequence 35, Application US/08483695
: Patent No. 5866139
: GENERAL INFORMATION:
: APPLICANT: Brechot, Christian
: APPLICANT: Krensdorf, Dina
: APPLICANT: Porchon, Colette
: TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
: TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
: TITLE OF INVENTION: Applications
: NUMBER OF SEQUENCES: 46
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1300 I Street, N.W.
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/483,695
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/965,285
: FILING DATE: 18-MAR-1993
: APPLICATION NUMBER: FR 91 06 882
: FILING DATE: 06-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Kenneth J.
: REGISTRATION NUMBER: 25,146
: REFERENCE/DOCKET NUMBER: 05286-0001-00000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-408-4000
: TELEFAX: 202-408-4400
: INFORMATION FOR SEQ ID NO: 35:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1210 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Other

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RESULT 5
US-07-965-285-35
; Sequence 35, Application US/07965285
; Patent No. 5879904
; GENERAL INFORMATION:
; APPLICANT: Brecht, Christian
; APPLICANT: Krensdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; NUMBER OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,285
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 06 882
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1210 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; DESCRIPTION: cDNA to genomic RNA
US-07-965-285-35

Alignment Scores:
Pred. No.: 6.65e-143 Length: 1210
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservatives: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 2 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-07-965-285-35 (1-1210)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 122 GTGCTGCTGCTATTTGCCGCGTC-----GACGCGGAACCCACGCTCAC 166
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerGlyPheValSerGlyAlaProGlyAlaLys 50
Db 167 GGGGGAAGTCCGCGGCACACTGTCTGATTGTTAGCTCTCGCACGCGCCACG 226
QY 51 GlnAsnValGlnLeuLeuAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 227 CAGAACGTCACGTCATCAACACCAACGCGCAGTTGGCACTCAATAGCAGCGCTCTGAC 286
QY 71 CysAsnAppSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheThrHisHisLysPheAsn 90

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Db 287 TGCATGATAGCTTAACACCGCTGTTGGCAGGCTTTTCTATCACCACCAAGTTCAAC 346
QY 91 SerSerGlyCysProGluAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 347 TCTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCCGATTTTGACCAAGGC 406
QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 407 TGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGACGCGCCCTACTGCTGGCAC 466
QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 467 TACCCCCCAAAACCTTTCGGTATTGTGCCCGGAGAGTGTGTGCTGCGGTATATTGC 526
QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 527 TTCACCTCCCGCCCGCTGTGTGGAGACGACGAGTCGGCGCGCGCCACCTACAGC 586
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 587 TGGGGTGAATAATGATACGAGCGCTTCGTCTTAACAATACCGAGGCCACCGCTGGGCAAT 646
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 647 TGGTTCCGTTGTACCTGGATGAACCACTGGATTTCACCAAAAGTGTGCGGAGCGCTCCT 706
QY 211 CysValIleGlyValAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 707 TGTGTATCGAGGGGGCGGCAACACCCCTGCACTGCCCTCCCTGATGTTGCTCCCAAG 766
QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 767 CATCCGAGCGCCACATACCTCTCGGTGGGCTCCGCTCCCTGGATCACACCCAGTGCCTG 826
QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 827 GTCGACTACCCGTATAGGCTTTGGCATTTATCCTTGTACCATCAACTACCATATTATAA 886
QY 271 IleArgMetTyrValGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
Db 887 ATCAGATGTAGTGGAGGGGTGCAACACAGCTGGAAAGCTGCCCTGCAACTGGACGCGG 946
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 947 GCGCAACGTTGCGATCTGGAGACAGGACAGCTCCGAG 985

RESULT 6
US-08-487-231-35
; Sequence 35, Application US/08487231
; Patent No. 5919454
; GENERAL INFORMATION:
; APPLICANT: Brecht, Christian
; APPLICANT: Krensdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; NUMBER OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,231

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647	TGTTCCGTTGTACCTGGATGAACCTCAACTGGATTACCAAAGTGTGCGGAGCGCCTCCT	705
211	CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys	230
707	TGTGTATCATCGAGGGGGGGGCAACACACCTGCATGCCCCCACTGATTGCTTCCGCAAG	765
231	HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu	250
767	CATCCGAGCGCCACATACCTCTCGTGGCTCGCTGGATCACACCCAGGTGCTG	826
251	ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys	270
827	GTCGACTACCGGTATAGGCTTTGGCATTTATCCTTGTACCATCACTACCATATTTAAA	886
271	IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaLaCysAsnTrpThrArg	290
887	ATCAGGATGTACGTGGAGGGGTGGAACACAGGCTGGAAGTGCCTGCNACTGGACGGG	946
291	GlyGluArgCysAspLeuGluAspArgAspArgSerGlu	303
947	GGCGACGTTGGCATCTGGGAAGACAGGACAGGTCGGAG	985

RESULT 7

US-09-201-912-35

; Sequence 35, Application US/09201912  
; Patent No. 6210962  
; GENERAL INFORMATION:  
; APPLICANT: Brechot, Christian  
; APPLICANT: Kremsdorf, Dina  
; APPLICANT: Porchon, Colette  
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a  
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic  
; TITLE OF INVENTION: Applications  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/201,912  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,285  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 05286-0001-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1210 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
; DESCRIPTION: CDNA to genomic RNA  
US-09-201-912-35  
Alignment Scores:

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Pred. No.: 6,65e-143 Length: 1210
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 3 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-09-201-912-35 (1-1210)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 122 GTGCTGCTGCTATTTGCCGGCGTC-----GACCGGAACCCACGTCACC 166

QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 167 GGGGGAAGTCCCGCCACACTGTGTCTGGATTGTTAGCTCTCTGCACCGCGCCAG 226

QY 51 GlnAsnValGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 70
Db 227 CAGAAGCTCAGCTGATCAACACCAACGGCAGTTGGCAGCTCAATAGCAGCGCTCTGAAC 286

QY 71 CysAsnAspSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 90
Db 287 TGCATATGATAGCTTAAACCGGCTGTTGGCAGGCTTTTCTATCACCACAGTTTCAAC 346

QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 347 TCTTCAGGCTGCTCTCAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTGACACGAGC 406

QY 111 TrpGlyProLeuSerTyrAlaLeuGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 407 TGGGGCCCTATCAGTTATGCAACGGAAGCGGCCCGACGAGCGCCCTACTGCTGGCAC 466

QY 131 TyrProProLysProCysGlyLeuValProAlaLysSerValCysGlyProValTyrCys 150
Db 467 TACCCCCCAACCTTGGGATTTGTCGGTATGTCGGCGAAGAGTGTGTGCTCGGTATATTC 526

QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 527 TTTCACTCCACGCCCCGTGTTGGTGGGAACGACGACGAGCTGGCGCGCCACCTACAGC 586

QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProLeuGlyAsn 190
Db 587 TGGGGTGAATAATGATACGAGCTCTTCGTCCTTAAACATACCGAGCCACCGCTGGGCAAT 646

QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 647 TGGTTCGGTTTACCTTGGATGAACCTCACTGGATTCCCAAGTGTGGGAGCGCTCTCT 706

QY 211 CysValIleGlyAlaGlyAlaGlyAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 707 TGTGTCATCGAGGGGCGGGCAACACACCTGCACCTGCCACCTGATGCTTCGCGAAG 766

QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 767 CATCCGAGCCACATCTCTCGGTCCGGCTCCGGTCCCTGGATCACACCGAGTGCCTG 826

QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 827 GTGCACTACCGGTATAGGCTTTGGCATATCTCTGTGACCATCAACTACACCATATTTAA 886

QY 271 IleArgMetTyrValGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
Db 887 ATCAGATGTAGTGGAGGGGTGGAACACAGCTGGAAGCTGCTGCAACTGGAGCGG 946

QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 947 GCGCAACGTTGGCATCTGGAAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 985

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RESULT 8

US-08-824-057-4

; Sequence 4, Application US/08824057

; Patent No. 6121020

```

; GENERAL INFORMATION:
; APPLICANT: SELBY, MARK
; APPLICANT: HOUGHTON, MICHAEL
; TITLE OF INVENTION: NOVEL HEPATITIS C E1 AND E2 TRUNCATED
; TITLE OF INVENTION: POLYPEPTIDES AND METHODS OF OBTAINING THE SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,057
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,959
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: McClung, Barbara G.
; REGISTRATION NUMBER: 33,113
; REFERENCE/DOCKET NUMBER: 0987,001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1989 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-824-057-4

```

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Alignment Scores:
Pred. No.: 1,38e-142 Length: 1989
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 3 Gaps: 1

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US-10-715-665-7\_COPY\_1\_303 (1-303) x US-08-824-057-4 (1-1989)

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QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 31 GTGCTGCTGCTATTTGCCGGCGTC-----GACCGGAACCCACGTCACC 75

QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 76 GGGGGAAGTCCCGCCACACTGTGTCTGGATTGTTAGCTCTCTGCACCGCGCCAG 135

QY 51 GlnAsnValGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 70
Db 136 CAGAAGCTCAGCTGATCAACACCAACGGCAGTTGGCAGCTCAATAGCAGCGCTTGAAC 195

QY 71 CysAsnAspSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 90
Db 196 TGCATATGATAGCTTAAACCGGCTGTTGGCAGGCTTTTCTATCACCACAGTTTCAAC 255

QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 256 TCTTCAGGCTGCTCTCAGAGGCTAGCCAGCTGCGAGCCCTTACCGATTGACACGAGC 315

QY 111 TrpGlyProLeuSerTyrAlaLeuGlySerGlyProAspGlnArgProTyrCysTrpHis 130

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;
; LENGTH: 1989 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-415-582-4

Alignment Scores:
Pred. No.: 1.38e-142 Length: 1989
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservativeness: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
Gaps: 3

US-10-715-665-7_COPY_1_303 (1-303) x US-09-415-582-4 (1-1989)

Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 31 GTGCTGCTGCTATTGTCGGCGGTC-----GACGGGGAACCCACGTCACC 75

Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyValAla 50
Db 76 GGGGAAAGTGGCGCCACACTGTGTCTGGATTGTTAGCCTCCTCGCACCGGCCCAAG 135

Qy 51 GlnAenValGlnLeuLeuAenThrAsnGlySerTrpHisLeuAenSerThrAlaLeuAsn 70
Db 136 CAGAACGTCCAGCTGATCAACCAACCGGCAAGTGGCACCTCAATAGCACGGCCCTGAAC 195

Qy 71 CysAsnAspSerLeuAenThrGlyTrpLeuAlaGlyLeuPheTyrHisHisPheAsn 90
Db 196 TGCAATGATAGCTCAACACCGGCTGGTGGCAGGCTTTCTATCATCACCAAGTTCAAC 255

Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 256 TCTTCAGGCTGTCTGAGAGCTAGCCAGCTGCGGACCCCTTACCGATTTCACCGAGGC 315

Qy 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 316 TGGGGCCCTATCAGTTATGCCAACGGAAAGCGGCCCCGACCGGCCCCCTACTGCTGGCAC 375

Qy 131 TyrProProLysProCysGlyIleValProLalysSerValCysGlyProValTyrCys 150
Db 376 TACCCCCCAAAACCTTGGCGTATTGTGCCCGGAAAGAGTGTGTGGTCCGGTATATTGC 435

Qy 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 436 TTCACCTCCAGCCCGCTGGTGGTGGGAAACGACCGACAGGTGGGCGGCCACCTACAGC 495

Qy 171 TrpGlyGluAenAspThrAspValPheValLeuAenAsnThrArgProProLeuGlyAsn 190
Db 496 TGGGGTGAAATGATATACGACGCTTCCTCTTAACAATACACAGCCACCGCTGGGCAAT 555

Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 556 TGGTTTCGGTTGTACCTGGATGAATCAACTGGATTTCACAAAGTGTGGCGAGCGCTCTCT 615

Qy 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 616 TGTGTGTCATCGGAGGGGCGGGCAACACCCCTGCACTGCCCCCAGTGTGCTTCGCCAAG 675

Qy 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTyrPheThrProArgCysLeu 250
Db 676 CATCCGGACGCCACATACCTCTCGGTGGGCTCCGGTCCCGTCCCTGGATCACACCGAGTGCCTG 735

Qy 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 736 GTCGACTACCCGTTATAGGCTTTGGCATTTATCTCTGTACCATCAACTACATATATTAA 795

Qy 271 IleArgMetTyrValGlyValGluHisArgLeuGluAlaAalaCysAsnTrpThrArg 290
Db 796 ATCAGGATGTACGTGGGAGGGGTGCAGACAGGCTGGAAAGCTGCCTGCAACTGGACGCGG 855

Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 856 GCGCAACGTTGGATCTGGAAGTAGGACAGGTCGAG 894

RESULT 9
US-09-415-582-4
; Sequence 4, Application US/09415582
; Patent No. 6326171
; GENERAL INFORMATION:
; APPLICANT: SELBY, MARK
; HOUGHTON, MICHAEL
; TITLE OF INVENTION: NOVEL HEPATITIS C E1 AND E2 TRUNCATED
; POLYPEPTIDES AND METHODS OF OBTAINING THE SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/415,582
; FILING DATE: 08-Oct-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: HARBIN, ALISA A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0987.006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2708
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

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;
; LENGTH: 1989 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-415-582-4

Alignment Scores:
Pred. No.: 1.38e-142 Length: 1989
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservativeness: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
Gaps: 3

US-10-715-665-7_COPY_1_303 (1-303) x US-09-415-582-4 (1-1989)

Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 31 GTGCTGCTGCTATTGTCGGCGGTC-----GACGGGGAACCCACGTCACC 75

Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyValAla 50
Db 76 GGGGAAAGTGGCGCCACACTGTGTCTGGATTGTTAGCCTCCTCGCACCGGCCCAAG 135

Qy 51 GlnAenValGlnLeuLeuAenThrAsnGlySerTrpHisLeuAenSerThrAlaLeuAsn 70
Db 136 CAGAACGTCCAGCTGATCAACCAACCGGCAAGTGGCACCTCAATAGCACGGCCCTGAAC 195

Qy 71 CysAsnAspSerLeuAenThrGlyTrpLeuAlaGlyLeuPheTyrHisHisPheAsn 90
Db 196 TGCAATGATAGCTCAACACCGGCTGGTGGCAGGCTTTCTATCATCACCAAGTTCAAC 255

Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 256 TCTTCAGGCTGTCTGAGAGCTAGCCAGCTGCGGACCCCTTACCGATTTCACCGAGGC 315

Qy 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 316 TGGGGCCCTATCAGTTATGCCAACGGAAAGCGGCCCCGACCGGCCCCCTACTGCTGGCAC 375

Qy 131 TyrProProLysProCysGlyIleValProLalysSerValCysGlyProValTyrCys 150
Db 376 TACCCCCCAAAACCTTGGCGTATTGTGCCCGGAAAGAGTGTGTGGTCCGGTATATTGC 435

Qy 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 436 TTCACCTCCAGCCCGCTGGTGGTGGGAAACGACCGACAGGTGGGCGGCCACCTACAGC 495

Qy 171 TrpGlyGluAenAspThrAspValPheValLeuAenAsnThrArgProProLeuGlyAsn 190
Db 496 TGGGGTGAAATGATATACGACGCTTCCTCTTAACAATACACAGCCACCGCTGGGCAAT 555

Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 556 TGGTTTCGGTTGTACCTGGATGAATCAACTGGATTTCACAAAGTGTGGCGAGCGCTCTCT 615

Qy 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 616 TGTGTGTCATCGGAGGGGCGGGCAACACCCCTGCACTGCCCCCAGTGTGCTTCGCCAAG 675

Qy 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTyrPheThrProArgCysLeu 250
Db 676 CATCCGGACGCCACATACCTCTCGGTGGGCTCCGGTCCCGTCCCTGGATCACACCGAGTGCCTG 735

Qy 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 736 GTCGACTACCCGTTATAGGCTTTGGCATTTATCTCTGTACCATCAACTACATATATTAA 795

Qy 271 IleArgMetTyrValGlyValGluHisArgLeuGluAlaAalaCysAsnTrpThrArg 290
Db 796 ATCAGGATGTACGTGGGAGGGGTGCAGACAGGCTGGAAAGCTGCCTGCAACTGGACGCGG 855

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Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
Db 856 GCGGAACGTTGCGATCTGGAAGATAGGACACAGGTCGCGAG 894

## RESULT 10

US-09-693-596-3  
; Sequence 3, Application US/09693596  
; Patent No. 6521423  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Michael  
; APPLICANT: Choo, Qui-Lim  
; APPLICANT: Abrignani, Sergio  
; APPLICANT: Chien, David  
; APPLICANT: Selby, Mark  
; APPLICANT: Glazer, Edward  
; TITLE OF INVENTION: Intracellular Production of Hepatitis C E1 and E2  
; FILE REFERENCE: 1378.002  
; CURRENT APPLICATION NUMBER: US/09/693,596  
; CURRENT FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/073,406  
; PRIOR FILING DATE: 1998-05-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1989  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1989)  
US-09-693-596-3

## Alignment Scores:

Pred. No.: 1.38e-142 Length: 1989  
Score: 1620.50 Matches: 283  
Percent Similarity: 96.93% Conservative: 1  
Best Local Similarity: 96.59% Mismatches: 4  
Query Match: 92.81% Indels: 5  
DB: 4 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x US-09-693-596-3 (1-1989)

Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
Db 31 GTCTGCTGCTATTGCGCGCTC-----CAGCGGGAACCCAGCTCACC 75  
Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
Db 76 GGGGGAAGTCCGGCCACACTGTCTGATTTGTAGCTCTCTCGCACCAGCGGCCAAG 135  
Qy 51 GluAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
Db 136 CAGAAGCTCAGCTGATCAACACACCGCAGTGGCACCTCAATAGCAGCGCCCTGAAC 195  
Qy 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTrpHisLysPheAsn 90  
Db 196 TGCATGATAGCTCAACACCGCTGTTGGCAGGGCTTTCTATCAACCAAGTTCAAC 255  
Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
Db 256 TCTTCAGGCTGCTCTGAGAGGCTAGCCAGCTGCGGACCCCTTACCGATTTTGACCGGCG 315  
Qy 111 TrpGlyProIleSerTrpAlaAsnGlySerGlyProAspGlnArgProTrpCysTrpHis 130  
Db 316 TGGGGCCCTATCAGTTATGCAACGGAAGCGGCGCCGACAGCGGCCCTACTCTGTCGAC 375  
Qy 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
Db 376 TACCCCAAAACCTTGGGTATTTGCGCGGAGAGTGTGTGTCGGGTATATTC 435  
Qy 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170

Db 436 TTCACCTCCAGCCCGTGGTGGGAACGACAGGTCGGGCGGCCCCACCTACAGC 495  
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProLeuGlyAsn 190  
Db 496 TGGGGTGAAATGATACGGACGCTTCGTCTTAAACAATACCGCCACCGCTGGCAAT 555  
Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
Db 556 TGGTTCGTTGTACCTGGATGAACCTCACTGGATTACCAAGTGTGGGAGCGCCCTCCT 615  
Qy 211 CysValIleGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
Db 616 TGTGTATCATCGAGGGCGGCAACACACCTGCACTGCCCTGCTGTTGTTCCGCAAG 675  
Qy 231 HisProAspAlaThrTrpSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
Db 676 CATCCGACCCACATCTCTCGTGGGCTCCGGTCCCTGGATCACCCAGGTGCTG 735  
Qy 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
Db 736 GTCGACTACCCGTATAGGCTTTGGCATTATCTTGTACCATCACTACACCATATTTAA 795  
Qy 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaLysAsnTrpThrArg 290  
Db 796 ATCAGGATGTACGTGGAGGGTGAACACAGGCTGGAAGCTGCTGCAACTGGACGCG 855  
Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
Db 856 GCGGAACGTTGCGATCTGGAAGATAGGACAGGTCGCGAG 894

RESULT 11  
US-08-444-818-88  
; Sequence 88, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Rutter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508)359-3876  
; TELEFAX: (508)359-3885  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8316 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..8316
US-08-444-818-88

Alignment Scores:
Pred. No.: 1,14e-141 Length: 8316
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 3 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-08-444-818-88 (1-8316)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 778 GTGCTGCTGCTATTTGCCGGCGTC-----GACGCGGAACCCACGTCACC 822
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 823 GGGGGAAGTCCCGCCACACTGTGTCTGGATTGTGTAGCTCTCTCGCACCGCGCCAAAG 882
QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 883 CAGAAGCTCAGCTGATCAACCAACGAGGTGGCACCTCAATAGCACGGCCCTGAAC 942
QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90
Db 943 TGCATATGATAGCTCAACACCGGCTGTTGGCAGGCGCTTTCTATCACCAAGTTCAAC 1002
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1003 TCTTACAGGCTGCTCAGAGGCTAGCCAGCTGCGGACCCCTTACCGATTTTGACCAAGGC 1062
QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 1063 TGGGGCCCTATCAGTTATGCCAACGGAAGGCGCCCGACGAGCGCCCTACTGCTGGCAC 1122
QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 1123 TACCCCCCAAAACCTTTGCGGTATTGTGCGCGGAGAGTGTGTGGTCCGGTATATTGC 1182
QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 1183 TTCACCTCCAGCCCCGTGTGTGGGAAACGACGACGAGTGGCGCGCCCACTACAGC 1242
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1243 TGGGGTGAAAATGATACGGACGCTCTTCGTCCTTAACATACGAGGCCCGCTGGGCAAT 1302
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 1303 TGGTTTCGGTTGTACCTGGATGAACCTCAACTGGATTACCAAGTGTGCGAGCGCTCCT 1362
QY 211 CysValIleGlyAlaGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 1363 TGTGTCTATCGAGGGGCGGCAACACCTCTGACTGCGCCCACTGATTGCTTCCGCAAG 1422
QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 1423 CATCCGAGCCCACTACTCTCGGTGGGCTCCGGTCCCGTCCCTGGATCAACCCAGTGCCTG 1482
QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 1483 GTCGACTACCGTATAGGCTTTGCAATTATCTTTGTACCATCAACTACACCATATTTAAA 1542
QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaCysAsnTrpThrArg 290
Db 1543 ATCAGGATGTACGTGGAGGGGTGGAACACAGGCTCGAAAGCTCGCTGCAACTGGACGCG 1602
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
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Db 1285 TGCAATGATAGCCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCACCACCAAGTTCAAC 1344  
Qy 91 SerSerGlyCysProGluAatGLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
Db 1345 TCITCAGGCTGCTCTGAGAGCTAGCAGCTGCCGACCCCTTACCGATTTCAGCAGGGC 1404  
Qy 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
Db 1405 TGGGGCCCTATCAGTTATGCAACCGAAGCGGCCCGCCAGCCAGCGCCCTACTGCTGGCAC 1464  
Qy 131 TyrProProLysProCysGlyValProAlaLysSerValCysGlyProValTyrCys 150  
Db 1465 TACCCCAAAACCTTCGGGTATTTGTCGCCGGAAGAGTGTGTGTCGGTATATTC 1524  
Qy 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
Db 1525 TTCACTCCAGCCCCGTGGTGGGAACGACGACAGGTCCGGCGGCCCACTACAGC 1584  
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
Db 1585 TGGGGTGAAATGATACGAGCGTCTTCGTCCTTAACAATACAGGCCACCGCTGGGCAAT 1644  
Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
Db 1645 TGGTTCGGTGTGACCTGGATGAATCAACTGGGATTCACCAAGGTGCGGAGCGCCTCCT 1704  
Qy 211 CysValIleGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
Db 1705 TGTGTATCGAGGGGGCGGCACACACCTCGACTGCCCCCACTGATTCCTTCCGCAAG 1764  
Qy 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
Db 1765 CATCCGAGCCACATACTCTCGGTGGGCTCCGCTCCCTGGATCACACCAGGTGCCTG 1824  
Qy 251 ValAspTyrProTyrArgLeuThrHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
Db 1825 GTGCACTACCGGTATAGGCTTTGGCATATTCCTTGTACCATCAACTACACATATTTAA 1884  
Qy 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
Db 1885 ATCAGATGTACTGGAGGGGTGCAACACAGCTGGAGCTGCACTGCACTGCACTGCGG 1944  
Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
Db 1945 GCGCAACGTTGCGATCTGGAAGACAGGACAGGTCCGAG 1983

RESULT 13

US-08-444-818-122  
; Sequence 122, Application US/08444818  
; Patent No. 6150087  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Y.  
; APPLICANT: Ruter, William J.  
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
; NUMBER OF SEQUENCES: 777  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,818  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,590

; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Harbin, Alisa A.  
; REGISTRATION NUMBER: 33,895  
; REFERENCE/DOCKET NUMBER: 0110.002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508)359-3876  
; TELEFAX: (508)359-3885  
; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9185 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-444-818-122  
  
Alignment Scores:  
Pred. No.: 1,32e-141 Length: 9185  
Score: 1620.50 Matches: 283  
Percent Similarity: 96.93% Conservative: 1  
Best Local Similarity: 96.59% Mismatches: 4  
Query Match: 92.81% Indels: 5  
DB: 3 Gaps: 1  
  
US-10-715-665-7\_COPY\_1\_303 (1-303) x US-08-444-818-122 (1-9185)  
Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
Db 1439 GTGCTCTGCTATTTTCCCGCGGTC-----GACGCGAAACCCACGTCAAC 1483  
Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
Db 1484 GGGGGAGGTGCCCGCCACACTGTGTCTGGATTGTAGCTCTCTCGCACCGGCGCCAG 1543  
Qy 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
Db 1544 CAGAACGTCAGCTGATCAACACCAACGCGAGTTGGCACCCTCAATAGCAGCGCCCTGAAC 1603  
Qy 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90  
Db 1604 TGCAATGATAGCTCAACACCGCGCTGGTTGGCAGGGCTTTTCTATCACCACAAAGTTCAAC 1663  
Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
Db 1664 TCTTCAGGCTGTCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCAGTTTTCACAGGGC 1723  
Qy 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
Db 1724 TGGGGCCCTATCAGTTATGCAACGGAAGCGGCCCGCCAGCCAGCGCCCTACTGCTGGCAC 1783  
Qy 131 TyrProProLysProCysGlyValProAlaLysSerValCysGlyProValTyrCys 150  
Db 1784 TACCCCAAAACCTTCGGGTATTTGTCGCCGGAAGAGTGTGTGTCGGTATATTC 1843  
Qy 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
Db 1844 TTCACCTCCAGCCCCGTGGTGGGAACGACGACAGGTCCGGCGGCCCACTACAGC 1903  
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
Db 1904 TGGGGTGAAATGATACGAGCGTCTTCGTCCTTAAACAATACAGGCGCACCGCTGGGCAAT 1963  
Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
Db 1964 TGGTTCGGTGTACCTGGATGAACCACTGGAATTCCACAAAGTGTGCGGAGCGCCTCCT 2023  
Qy 211 CysValIleGlyValGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
Db 2024 TGTGTATCGAGGGGGCGGCACACACCTTCGACTGCCCTCCACCTGATTTGCTTCCGCAAG 2083  
Qy 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250

Db 2084 CATCGGACGCCACATACCTCTCGGTCCGGCTCGGTCCCTGGATCACACCCAGGTGCCTG 2143  
 QY 251 ValAspTyrProTyrArgLeuThrHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 Db 2144 GTGAGTACCCGTATAGGCTTTGGCAATATCTTGTACCATCAACTACACCATATTTAAA 2203  
 QY 271 IleArgMetTyrValGlyValGlyValGluHisArgLeuGluAlaAlaCysAsnTyrThrArg 290  
 Db 2204 ATCAGGATGTACGTGGAGGGGTGCAACACAGGCTGGAAGCTGCCTGCAACTGGACGGG 2263  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 Db 2264 GCGCAACGTGTGGATCTGGAACACAGGACAGGTCCGAG 2302

RESULT 14  
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 ; Sequence 123, Application US/08444818  
 ; Patent No. 6150087  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chien, David Y.  
 ; APPLICANT: Rutter, William J.  
 ; TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
 ; NUMBER OF SEQUENCES: 777  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Chiron Corporation  
 ; STREET: 4560 Horton Street  
 ; CITY: Emeryville  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94608-2916  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/444,818  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/403,590  
 ; FILING DATE: 14-MAR-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Harbin, Alisa A.  
 ; REGISTRATION NUMBER: 33,895  
 ; REFERENCE/DOCKET NUMBER: 0110.002  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (508)359-3876  
 ; TELEFAX: (508)359-3885  
 ; INFORMATION FOR SEQ ID NO: 123:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9185 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; ANTI-SENSE: YES  
 ; US-08-444-818-123

Alignment Scores:  
 Pred. No.: 1-32e-141 Length: 9185  
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 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: 3 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x US-08-444-818-123 (1-9185)

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 QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
 Db 7642 CAGAAGCTCCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCACGCGCCCTGAAC 7583  
 QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90  
 Db 7582 TGCATATAGTACCTCAACACCGGCTGTTGGCAGGGCTTTTCTATATCACCAAGTTCAC 7523  
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 QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
 Db 7462 TGGGCGCCCTATCAGTTATGCCAAGCGAGCGGCCCGACAGCGGCCCTACTGCTGGCAC 7403  
 QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
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 QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
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 ; Sequence 1, Application US/09388874  
 ; Patent No. 6284249  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Veronique Barban  
 ; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR  
 ; TITLE OF INVENTION: TREATING C HEPATITIS  
 ; FILE REFERENCE: PMCF97-03A  
 ; CURRENT APPLICATION NUMBER: US/09/388,874  
 ; EARLIER FILING DATE: 1999-09-02  
 ; EARLIER APPLICATION NUMBER: PCT/FR98/00448  
 ; EARLIER FILING DATE: 1998-03-06  
 ; EARLIER APPLICATION NUMBER: 97/02,887  
 ; EARLIER FILING DATE: 1997-03-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSeq for Windows Version 3.0

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; LENGTH: 9379  
; TYPE: DNA  
; ORGANISM: Virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (320)...(9352)  
US-09-388-874-1

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Pred. No.: 1.36e-141 Length: 9379  
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Percent Similarity: 96.93% Conservative: 1  
Best Local Similarity: 96.59% Mismatches: 4  
Query Match: 92.81% Indels: 5  
DB: 3 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x US-09-388-874-1 (1-9379)

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Qy 51 GluAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 1544 CAGAACGTCAGCTGATCAACACCAACGCGAGTGGCACCTCAATAGCAGGCCCTGAAC 1603
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Db 2204 ATCAGGATGTACGTGGGAGGGTGAACACACAGGCTGGAAGCTGCTGCACTGGACGGG 2263  
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Search completed: April 15, 2005, 09:09:35  
Job time : 215 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 15, 2005, 08:04:43 ; Search time 1564 Seconds

(without alignments)  
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Title: US-10-715-665-7\_COPY\_1\_303

Perfect score: 1746

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Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1620.5	92.8	1914	15	US-10-187-257-3 Sequence 3, Appli
2	1620.5	92.8	1914	16	US-10-265-083-1 Sequence 1, Appli
3	1620.5	92.8	1989	17	US-10-371-040-3 Sequence 3, Appli
4	1620.5	92.8	9379	9	US-09-916-359-1 Sequence 1, Appli
5	1620.5	92.8	9401	18	US-10-445-724-1 Sequence 1, Appli
6	1623.5	87.3	9646	9	US-09-742-659-3 Sequence 3, Appli
7	1521.5	87.1	9416	9	US-09-238-076-19 Sequence 19, Appl
8	1521.5	87.1	9416	10	US-09-995-937-19 Sequence 19, Appl
9	1521.5	87.1	9416	10	US-09-917-563-19 Sequence 19, Appl
10	1521.5	87.0	9622	18	US-10-475-988-2 Sequence 2, Appli
11	1518.5	87.0	9365	10	US-09-827-688-7 Sequence 7, Appli
12	1515.5	86.8	9646	9	US-09-238-076-1 Sequence 1, Appli
13	1515.5	86.8	9646	10	US-09-995-937-1 Sequence 1, Appli
14	1515.5	86.8	9646	10	US-09-917-563-1 Sequence 1, Appli
15	1515.5	86.8	12980	9	US-09-238-076-5 Sequence 5, Appli
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18	1512.5	86.6	1845	17	US-10-365-620-73 Sequence 73, Appl
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21	1512.5	86.6	2517	19	US-10-912-969-77 Sequence 77, Appl
22	1512.5	86.6	2517	19	US-10-913-171-48 Sequence 48, Appl
23	1512.5	86.6	9599	17	US-10-189-359-13 Sequence 13, Appl
24	1512.5	86.6	10803	9	US-09-747-419-17 Sequence 17, Appl
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28	1503	86.1	1938	19	US-10-913-969-73 Sequence 73, Appl
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38	1371	78.5	834	19	US-10-488-269A-6 Sequence 6, Appli
39	1324.5	75.9	9275	15	US-10-259-275-39 Sequence 39, Appl
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C 41	1317	75.4	7927	16	US-10-128-587A-32 Sequence 32, Appl
C 42	1317	75.4	7927	17	US-10-128-588B-32 Sequence 32, Appl
43	1313.5	75.2	3730	17	US-10-128-590-22 Sequence 22, Appl
44	1313.5	75.2	3730	16	US-10-128-587A-22 Sequence 22, Appl
45	1313.5	75.2	3730	17	US-10-128-588B-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1  
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; Sequence 3, Application US/10187257  
; Publication No. US20030138458A1  
; GENERAL INFORMATION:  
; APPLICANT: HOUGHTON, Michael  
; APPLICANT: COATES, Steve  
; APPLICANT: O'HAGAN, Derek  
; TITLE OF INVENTION: HCV E1E2 VACCINE COMPOSITIONS  
; FILE REFERENCE: 2302-17206  
; CURRENT APPLICATION NUMBER: US/10/187,257  
; CURRENT FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1914  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HCV-1 E1/E2/p7 region

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Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 15 Gaps: 1

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DB 889 TGGGGCCCTATCAGTTATGCCAACGGAAGCGGGCCCGACAGCGCCCTCTGCTGGCAC 948
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Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 15 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-10-265-083-1 (1-1914)
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DB 604 GTGCTGCTGCTATTTGCCGGCGTC-----GACGCGGAACCCACGTCACC 648
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
DB 649 GGGGAAGTCCGGCCACACTGTGTCTGGATTGTGTAGCTCTCTCGCACAGCGCCAAAG 708
QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
DB 709 CAGAACGTCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCACGCGCCCTGAAC 768
QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTrpHisHisLysPheAsn 90
DB 769 TGCATGATAGCTCAACACCGGCTGTGTGGCAGGGCTTTTCTATCACCAACGATTCAC 828
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
DB 829 TCTTCAAGCTGTCTGAGAGGCTAGCCAGCTGCGCAGCCCTTACCGATTTCACACAGGC 888
QY 111 TrpGlyProIleSerTrpAlaAsnGlySerGlyProAspGlnArgProTrpHisHis 130
DB 889 TGGGGCCCTATCAGTTATGCCAACGGAAGCGGGCCCGACAGCGCCCTCTGCTGGCAC 948
QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
DB 949 TACCCCCCAAACTTTGCGGTATTGTGCCCGGAGAGGTGTGTGGTCCGGTATATTGC 1008
QY 151 PheThrProSerProValValValGlyThrAspArgSerGlyAlaProThrHis 170
DB 1009 TTCACCTCCAGCCCCGCTGGTGGTGGGAACGACGACAGCTCGGCGCGCCACCTACAGC 1068
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
DB 1069 TGGGGGTGAAATGATACGAGACGCTCTTCGTCTCTTAAATACACGAGCCACCGCTGGCAAT 1128

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QY 191 TrrPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
 Db 1129 TGGTTTCGGTGTACCTGGATGAACCTCACTGGATTCAACAAAGTGTGGGAGCGCTCT 1188  
 QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
 Db 1189 TGTGTATCATCGAGGGGGGCAACACACCTGCACCTGCCCTCACTGATTCCTCCGCAAG 1248  
 QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 Db 1249 CATCCGAGCCGACATACCTCTGGTGGGCTCCGCTCCCTGGATCAACACCGAGTGGCTG 1308  
 QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 Db 1309 GTCCAGTACCCGTATAGGCTTGGCATATCTTGTACCACTCACTATATTTAAA 1368  
 QY 271 IleArgMetTyrValGlyGlyValGlyHisArgLeuGluAlaCysAsnTrpThrArg 290  
 Db 1369 ATCAGGATGTACGTGGGAGGGTGGACACAGGCTGGAGCTGCCTGCACCTGCAGCGCG 1428  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 Db 1429 GCGGACGTTGCCGATCTGGAGATAGGACAGGTCGCGAG 1467

RESULT 3

US-10-371-040-3  
 ; Sequence 3, Application US/10371040  
 ; Publication No. US20040001854A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Houghton, Michael  
 ; APPLICANT: Choo, Qui-Lim  
 ; APPLICANT: Abignani, Sergio  
 ; APPLICANT: Chien, David  
 ; APPLICANT: Selby, Mark  
 ; APPLICANT: Glazer, Edward  
 ; TITLE OF INVENTION: Intracellular Production of Hepatitis C E1 and E2  
 ; FILE REFERENCE: 1378.002  
 ; CURRENT APPLICATION NUMBER: US/10/371,040  
 ; CURRENT FILING DATE: 2003-02-18  
 ; PRIOR APPLICATION NUMBER: US/09/073,406  
 ; PRIOR FILING DATE: 1998-05-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/045,675  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-06  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1989  
 ; TYPE: DNA  
 ; ORGANISM: Hepatitis C virus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1989)  
 ; US-10-371-040-3

Alignment Scores:  
 Pred. No.: 8,11e-167 Length: 1989  
 Score: 1620.50 Matches: 283  
 Percent Similarity: 96.93% Conservative: 1  
 Best Local Similarity: 96.59% Mismatches: 4  
 Query Match: 92.81% Indels: 5  
 DB: 17 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x US-10-371-040-3 (1-1989)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
 Db 31 GTGCTGCTGCTATTTCGCGCGTC-----GACGCGAAACCCACGTCACC 75  
 QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
 Db 76 GGGGGAAGTCCCGGCCACACTGTGTGGATTGTGGCTCTCGCACGAGCGCCAAAG 135

QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
 Db 136 CAGAACGTCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCAGCGCTTGAAC 195  
 QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90  
 Db 196 TGCATATGATAGCTCAACACCGCTGTGGCAGGGCTTTTCTATATCACCAAGTTTCAAC 255  
 QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
 Db 256 TCTTTCAGCTGTCTCGAGAGGCTAGCAGCTGCCGCCCCCTTACCGATTTTTGACAGGGC 315  
 QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
 Db 316 TGGGGCCCTATCATAGTTATGCCAACGGAAGCGGCCCGCCCTACTGCTGGCAC 375  
 QY 131 TyrProProlyProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
 Db 376 TACCCCCCAAAACCTTTCGGGTATTGTGCCCGCGAAGAGTGTGTGTCGGTATATTGC 435  
 QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
 Db 436 TTCACCTCCAGCCCCGTGTGTGGGAACACGACGAGTGGGCGCGGCCACCTACAGC 495  
 QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
 Db 496 TGGGGTGAAATGATACGGAGAGTCTTCGTCCTTAAACAATACACGAGCCCGCTGGGCAAT 555  
 QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
 Db 556 TGGTTTCGGTGTACCTGGATGAACCTCACTGGATTTCACCAAGTGTGGGAGCGCTCTCT 615  
 QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
 Db 616 TGTGTCTATCGAGGGGGCGGCAACACCTGCACCTGCCCACTGATTCCTCCGCAAG 675  
 QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
 Db 676 CATCCGAGCCACATACCTCTCGGTGGGCTCGGTCCTGGATCAACCCAGGTGCTG 735  
 QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
 Db 736 GTCGATACCCGTATAGGCTTTGGCATTTATCTTGTACCATCACTACACCATATTAAA 795  
 QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaCysAsnTrpThrArg 290  
 Db 796 ATCAGGATGTACGTGGAGGGTGGAAACACAGCTGGAAAGCTGCTGCAACTGCAGCGCG 855  
 QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
 Db 856 GCGGACGTTGCCGATCTGGAAGATAGGACAGGTCGCGAG 894

RESULT 4

US-09-916-359-1  
 ; Sequence 1, Application US/09916359  
 ; Patent No. US2002003473A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Veronique Barban  
 ; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR  
 ; TITLE OF INVENTION: TREATING C HEPATITIS  
 ; FILE REFERENCE: PMCF97-03A  
 ; CURRENT APPLICATION NUMBER: US/09/916,359  
 ; CURRENT FILING DATE: 2001-07-26  
 ; PRIOR APPLICATION NUMBER: 09/388,874  
 ; PRIOR FILING DATE: 1999-09-02  
 ; PRIOR APPLICATION NUMBER: 97/02,887  
 ; PRIOR FILING DATE: 1997-03-06  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 9379  
 ; TYPE: DNA  
 ; ORGANISM: Virus

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (320)... (9352)
US-09-916-359-1

Alignment Scores:
Pred. No.: 6,02e-166 Length: 9379
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 9 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-09-916-359-1 (1-9379)
QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 1439 GTGCTGCTGCTATTTGCCGGCGTC-----GACGCGGAACCCACGTCACC 1483
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 1484 GGGGGAAGTCCGGCCACACTGTGCTGGATTGTTAGCTCTCGCACAGCGCCCAAG 1543
QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 1544 CAGAACGTCAGCTGATCAACCAACGCGAGTTGGCACCTCAATAGCACGCGCCCTGAAC 1603
QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheThrHisHisLysPheAsn 90
Db 1604 TGCAATGATAGCTCAACACCGCTGTTGGCAGGCGCTTTCTATCACCACAAGTTCAAC 1663
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1664 TCTTCAGGCTGCTCTGAGAGGCTAGCCAGCTGCGCAGCCCTTACCGATTTCACCGAGGC 1723
QY 111 TrpGlyProIleSerTrpAlaAsnGlySerGlyProAspGlnArgProTrpCysTrpHis 130
Db 1724 TGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGCACAGGCTCTCTAGTGGCAC 1783
QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 1784 TACCCCCCAAAACCTTTGCGGTATTGTCGCCGGAAGAGTGTGTGCTCGGTATATTGC 1843
QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTrpSer 170
Db 1844 TTCACCTCCAGCCCGCTGTGTGGGAACGACGACGAGTGTGGCGCGCCCACTACAGC 1903
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1904 TGGGGTGAANAATGATACGACGCTCTTCGTCCTTAAACATACACGACCGCTGGCAAT 1963
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 1964 TGCTTCGGTGTACCTGGATGAACCTCACTGGATTCAACAAAGTGTGCGGAGCGCTCCT 2023
QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 2024 TGTGTATCGAGGGGCGGGCAACAAACCTGCACTGCGGCTCGGTCCTGGATACACCCAGGTGC 2083
QY 231 HisProAspAlaThrTrpSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 2084 CATCCGAGCCACATACACTCTCGGTGGGCTCGGTCCTGGATACACCCAGGTGCCTG 2143
QY 251 ValAspTyrProTrpArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 2144 GTCGACTACCGGTATAGGCTTTGGCATTTATCCTTGATCATCAACTACACCATATTTAAA 2203
QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuLeuAlaLysAsnTrpThrArg 290
Db 2204 ATCAGATGTACGTGGAGGGGTGGAACACAGGCTGGAAGCTGCAACTGGACGCGG 2263
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303

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Db 2264 GCGGAACGTTGCGATCTCGAAGACAGGACAGGTCGGAG 2302
RESULT 5
US-10-445-724-1
; Sequence 1, Application US/10445724
; Publication No. US20040101829A1
; GENERAL INFORMATION:
; APPLICANT: STAPLETON, JACK T.
; APPLICANT: WUENSCHMANN, SABINA
; TITLE OF INVENTION: A PROTEIN THAT INTERACTS WITH LIPIDS AND
; FILE REFERENCE: IOWA:045US
; CURRENT APPLICATION NUMBER: US/10/445,724
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: 60/392,158
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9401
; TYPE: DNA
; ORGANISM: Hepatitis C virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (342).. (9374)
US-10-445-724-1

Alignment Scores:
Pred. No.: 6,03e-166 Length: 9401
Score: 1620.50 Matches: 283
Percent Similarity: 96.93% Conservative: 1
Best Local Similarity: 96.59% Mismatches: 4
Query Match: 92.81% Indels: 5
DB: 18 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-10-445-724-1 (1-9401)
QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 1461 GTGCTGCTGCTATTTGCCGGCGTC-----GACGCGGAACCCACGTCACC 1505
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 1506 GGGGGAAGTCCGGCCACACTGTGCTGGATTGTTAGCTCTCGCACGCGCCAAAG 1565
QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 1566 CAGAACGTCAGCTGATCAACCAACGCGAGTTGGCACCTCAATAGCACGCGCCCTGAAC 1625
QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheThrHisHisLysPheAsn 90
Db 1626 TGCAATGATAGGCTCAACACCGCTGGTTGGCAGGCGCTTTCTATCACCACAAGTTCAAC 1685
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1686 TCTTCAGGCTGCTCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTCACCGAGGC 1745
QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTrpCysTrpHis 130
Db 1746 TGGGGCCCTTATCAGTTATGCCAACGGAAGCGCGCCCGACGCGCCCTTACTGCTGGCAC 1805
QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 1806 TACCCCCCAAAACCTTGGGTATTGTCGCCGGAAGAGTGTGTGGTCCGATATTGCG 1865
QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTrpSer 170
Db 1866 TTCACCTCCAGCCCGCTGGTGGTGGGAACGACGACGAGTGGGCGCGCCACCTACAGC 1925
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1925 TGGGGTGAANAATGATACGAGCGCTCTTCGTCCTTAAACATACACGCGCCCGCTGGCAAT 1985

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QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
DB 1986 TGGTTCGGTGTACCTGGATGAACCTCAACTGGATTACCAAGGTGTGGAGCGCCTCCT 2045  
QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
DB 2046 TGTGTCACTCGAGGGGGGGGCAACCAACCCCTGCACCTGCCCTGATTTGCTCCGCAAG 2105  
QY 231 HisProAspAlaThrTrpSerArgCysGlySerGlyProTrpPheThrProArgCysLeu 250  
DB 2106 CATCCGAGCCACATACCTCGGTGGGCTCCGCTCCGTGGATCAACCCAGGTGCTG 2165  
QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
DB 2166 GTGACTACCGTATAGCTTTGGCAATTATCTTGTACCACTACACCATATTTAAA 2225  
QY 271 IleArgMetTyrValGlyGlyValGlyHisArgLeuGluAlaCysAsnTrpThrArg 290  
DB 2226 ATCAGGATGTACGTGGAGGGGTGCAACACAGGCTGGAAGCTGCTGCAACTGGACGCG 2285  
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
DB 2286 GCGCAACGTTGCGATCTGGAGACAGGACAGGTCCGAG 2324  
RESULT 6  
US-09-742-659-3  
; Sequence 3, Application US/09742659  
; Patent No. US20010034019A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong, Zhi  
; APPLICANT: Butkiewicz, Nancy J.  
; APPLICANT: Zhong, Weidong  
; APPLICANT: Ingravallo, Paul  
; APPLICANT: Wright-Minogue, Jacquelyn  
; APPLICANT: Lau, Johnson Y.  
; APPLICANT: Lemon, Stanley M.  
; TITLE OF INVENTION: Chimeric HCV/GBV-B viruses  
; FILE REFERENCE: ID01116  
; CURRENT APPLICATION NUMBER: US/09742,659  
; CURRENT FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: US 60/171,469  
; PRIOR FILING DATE: 1999-12-22  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
US-09-742-659-3  
Alignment Scores:  
Pred. No.: 2 56e-155 Length: 9646  
Score: 1523.50 Matches: 263  
Percent Similarity: 93.17% Conservative: 10  
Best Local Similarity: 89.76% Mismatches: 15  
Query Match: 87.26% Indels: 5  
DB: 9 Gaps: 1  
US-10-715-665-7\_COPY\_1\_303 (1-303) x US-09-742-659-3 (1-9646)  
QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
DB 1461 GTGCTGCTGCTATTGTCGGCGTC-----GACGCGGAACCCACGTCACC 1505  
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
DB 1506 GGGGGAAGTCCGGCCACACACCGCTGGCTGTTGCTCTCTTACACCGAGCGCAAG 1565  
QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70  
DB 1566 CAGAACATCACTGATCAACACCAACGCGAGTTGGCAGCATCAATAGCAGGCTTGAAC 1625  
QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisLysPheAsn 90

DB 1626 TGCATGAAGCCCTTAACACCGCTGGTAGCAGGCTCTTCTATCAGCACAAATTTCAAC 1685  
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
DB 1686 TCTTCAGCGTGTCTCGAGAGGTGGCCAGCTGCCGAGCGCTTACCGATTTTGGCCAGGCG 1745  
QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
DB 1746 TGGGTCTCTATCAGTTATGCCACGGAAGGGCCCTCAGCAGNACGCCCTACTGCTGGCAC 1805  
QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
DB 1806 TACCCTCAAAGACCTTGTGGCATTGTGCCGCAAGAGCGTGTGTGCCCGGTATATTGC 1865  
QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170  
DB 1866 TTCACCTCCAGCCCCCGTGGTGGGAACGACCGACAGGTGGGCGCGCTACCTACGACG 1925  
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
DB 1926 TGGGTGCAATGATACGGATGTCTGCTCTTNAACACACAGGCGCACCGCTGGGCAT 1985  
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
DB 1986 TGGTTCGGTGTACCTGGATGAACCTCAACTGGATTACCAAAAGTGTGGGAGCGCCCCC 2045  
QY 211 CysValIleGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230  
DB 2046 TGTGTCACTCGAGGGGTGGGCAACACACCTTGTCTGCCCCACTGATTGCTTCCGCAA 2105  
QY 231 HisProAspAlaThrTrpSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
DB 2106 CATCCGGAACCCACATACCTCTCGTGGCGGTCCGCTCCGTGGATTACCCAGGTGCGATG 2165  
QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
DB 2166 GTGACTACCGTATAGCTTTGGCATCTATCTTGTACCACTCAATTAACCATATTCAA 2225  
QY 271 IleArgMetTyrValGlyGlyValGlyHisArgLeuGluAlaCysAsnTrpThrArg 290  
DB 2226 GTCAGGATGTACGTGGAGGGGTGAGACAGGCTGGAAGCGGCTGCAACTGGACGCGG 2285  
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
DB 2286 GCGCAACGCTGTGATCTGGAGACAGGACAGGTCCGAG 2324  
RESULT 7  
US-09-238-076-19  
; Sequence 19, Application US/09238076  
; Patent No. US20020102540A1  
; GENERAL INFORMATION:  
; APPLICANT: RICE, CHARLES et al.  
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C  
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/238,076  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 09/034,756
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-09-238-076-19

Alignment Scores:
Pred. No.: 4,11e-155 Length: 9416
Score: 1521.50 Matches: 263
Percent Similarity: 92.83% Conservative: 9
Best Local Similarity: 89.76% Mismatches: 16
Query Match: 87.14% Indels: 5
DB: 9 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-09-238-076-19 (1-9416)

QY 11 ValLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 1461 GTGCTGCTGCTATTTCGCCGGCGTC-----GACGCGGAACCCACGCTCACC 1505

QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 1506 GGGGGAAGTCCCGCCACACACCGGCTGGCTTTGGTCTCTTACACGAGCGCCAAG 1565

QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpPheHisLeuAsnSerThrAlaLeuAsn 70
Db 1566 CAGAACATCACTGATCAACACCAACGCGCAGTTGGCATCATCAATAGCAGCGCTTGAAC 1625

QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyHisHisLysPheAsn 90
Db 1626 TGCACGATAGCCTTACACCGGCTGTTAGCAGGCGCTTCTTATCGCCACAAATTCAC 1685

QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1686 TCTTCAGGCTGCTCCTCAGAGGTTGGCCAGCTGCCGACGCTTACCGATTTCGCCAGGGC 1745

QY 111 TrpGlyProIleSerTyAlaAsnGlySerGlyProAspGlnArgProTyCysTrpHis 130
Db 1746 TGGGGTCCCATCATGTTATGCCAACGGAAGCGGCTTTGACGACGCGCCCTACTGTGGCAC 1805

QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyCys 150
Db 1806 TACCTTCCAGACCTTGTGGCATTGTCCCGCAAGAGCGTGTGTGCCCGGTATATTGC 1865

QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTySer 170
Db 1866 TTCACCTCCAGCCCCCGTGGTGGTGGGAACGACGACGAGTGGCGCGCTACCTACAGC 1925

QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1926 TGGGGTGCAAATGATACGATGCTTCCTCGTCTTTAAACAACACACGCGCCGCTGGGCAAT 1985

QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 1986 TGGTTCCGTTGTACCTTGGATGAATCACTGGAATTCACCAAGTGTGGGAGCGCCCCCT 2045

QY 211 CysValIleGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 2046 TGTGTATCGAGGGGTGGGCAACAACACCTTCTCTGCCCACTGATTGCTTCGCGCAA 2105

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QY 231 HisProAspAlaThrTySerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 2106 CATCCGAAGCCACATATCTTCGGTCCGCTCCGTCCTGGATTACACCGAGTGCATG 2165

QY 251 ValAspTyTrpTyArgLeuTrpHisTyProCysThrIleAsnTyThrIlePheLys 270
Db 2166 GTCGACTACCCGATAGGCTTTGGCACTATCTTGTACTATCAATTACACCATATTCAA 2225

QY 271 IleArgMetTyValGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
Db 2226 GTCAGGATGTACGTGGAGGGTGCAGCACAGCTGGAGCGCTGCAACTGGACGCG 2285

QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 2286 GCGGAACGCTGTGATCTGGAAGACAGGACAGGTCCGAG 2324

RESULT 8
US-09-995-937-19
; Sequence 19, Application US/09995937
; Publication No. US20030028010A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/995,937
; APPLICATION NUMBER: US/09/995,937
; FILING DATE: 28-No. US20030028010A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,756
; FILING DATE: 04-May-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-995-937-19

Alignment Scores:
Pred. No.: 4,11e-155 Length: 9416
Score: 1521.50 Matches: 263
Percent Similarity: 92.83% Conservative: 9
Best Local Similarity: 89.76% Mismatches: 16
Query Match: 87.14% Indels: 5
DB: 10 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-09-995-937-19 (1-9416)

QY 11 ValLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30

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Db 1461 GTGCTGCTGCTATTGGCGGCGTC-----GACGCGGAACCCACGTCACC 1505
Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuAlaProGlyAlaLys 50
Db 1506 GGGGGAAGTGGCGGACACACCGCTGGGCTTGTGCTCTTACACAGGCGCCAAG 1565
Qy 51 GlnAsnValGlnLeuLeuLeuAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 1566 CAGAACATCCAACATGATCAACACACGCGAGTTGGCACATCAATAGCAGGCTTGNAC 1625
Qy 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90
Db 1626 TGCAACATAGCTTACACCGGCTGTAGCAGGCTCTTCTATCGCCACAAATTCAC 1685
Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1686 TCCTCAGGCTGTCTGAGAGTTGGCAGCTGCCGAGCCTTACCGATTTCGCCAGGCG 1745
Qy 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 1746 TGGGTCCTCAAGACCTTGTGCATTTGTCGCGCAAGAGCGTGTGTGCGCGGTATATGC 1805
Qy 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 1806 TACCCTCCAAGACCTTGTGCATTTGTCGCGCAAGAGCGTGTGTGCGCGGTATATGC 1865
Qy 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 1866 TTCACTCCAGCCCCGCTGGTGGTGGGAGCAGCAGGTCGGCGCGCTTACCTACGAGC 1925
Qy 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1926 TGGGTCGCAATGATACGATGCTTCGTCCTTAAACACACGAGCCACCGCTGGGCAAT 1985
Qy 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 1986 TGGTTCGCTGTGTACCTGATGAACCTCACTGGATTACCAAGAGTGTGCGAGCGCCCT 2045
Qy 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 2046 TGTGTCATCGAGGGTGGGCAACACACCTTGTCTGCGCCCACTGATTGCTTCCGCAAA 2105
Qy 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 2106 CATCCGGAAGCCACATACTCTCGTGGGCTCCGCTCCCTGGATTACACCCAGGTGATG 2165
Qy 251 ValAspTyrProTyrArgLeuThrHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 2166 GTCGACTTACCCTGATAGGCTTTGGCACTATCCTTGTACTATCAATTACACATATTCAA 2225
Qy 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaLaCysAsnTrpThrArg 290
Db 2226 GTCAGGATGTGTTGGAGGGTTCGACAGGTCGAGGCTGGAAGCGGCTGCACCTGAG 2285
Qy 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 2286 GCGCAACGCTGTGATCTGGAAGACAGGACAGGTCGAG 2324
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## RESULT 9

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US-09-917-563-19
; Sequence 19, Application US/09917563
; Publication No. US20030073080A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
```

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; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,563
; FILING DATE: 27-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/238,076
; FILING DATE: 26-JAN-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9416 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-917-563-19
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## Alignment Scores:

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Pred. No.: 4 11e-155 Length: 9416
Score: 1521.50 Matches: 263
Percent Similarity: 92.83% Conservative: 9
Best Local Similarity: 89.76% Mismatches: 16
Query Match: 87.14% Indels: 5
DB: 10 Gaps: 1
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US-10-715-665-7\_COPY\_1\_303 (1-303) x US-09-917-563-19 (1-9416)

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Qy 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 1461 GTGCTGCTGCTATTGGCGGCGTC-----GACGCGGAACCCACGTCACC 1505
Qy 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 1506 GGGGGAAGTGGCGGACACACCGCTGGGCTTGTGCTCTTACACAGGCGCCAAG 1565
Qy 51 GlnAsnValGlnLeuLeuLeuAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 1566 CAGAACATCCAACATGATCAACACACGCGAGTTGGCACATCAATAGCAGGCTTGNAC 1625
Qy 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90
Db 1626 TGCAACATAGCTTACACCGGCTGTAGCAGGCTCTTCTATCGCCACAAATTCAC 1685
Qy 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1686 TCCTCAGGCTGTCTGAGAGTTGGCAGCTGCCGAGCCTTACCGATTTCGCCAGGCG 1745
Qy 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 1746 TGGGTCCTCAAGACCTTGTGCATTTGTCGCGCAAGAGCGTGTGTGCGCGGTATATGC 1805
Qy 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 1806 TACCCTCCAAGACCTTGTGCATTTGTCGCGCAAGAGCGTGTGTGCGCGGTATATGC 1865
Qy 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 1866 TTCACTCCAGCCCCGCTGGTGGTGGGAGCAGCAGGTCGGCGCGCTTACCTACGAGC 1925
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QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProIleuGlyAsn 190
DB 1926 TGGGGTGCAAAATGATACGGATGCTTCGTCTTAACAACACACAGGCCACCGCTGGGCAAT 1985
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
DB 1986 TGGTTCCGTTGTACCTGGATGAACCTCACTGGATTCCACCAAGTGTGCGAGCGCCCT 2045
QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
DB 2046 TGTGTCATCGAGGGGTGGCAACAACACTTGCTCTGCCCACTGATTGCTTCGCAAA 2105
QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
DB 2106 CATCGGAAGCCACATACTCTCGGTCCGCTCCGTCCTGGATTACACCCAGGTGCATG 2165
QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
DB 2166 GTCGACTACCGTATAGGCTTTGGCACTATCTTGTAATCAATACCATATATCAAA 2225
QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
DB 2226 GTCAGGATGTACGTGGAGGGTTCGAGCACAGCTGGAAGCGCCTGCAACTGGACGCG 2285
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
DB 2286 GCGGAACGCTGTGATCTGGAAGACAGGAGCAGGTCGAG 2324

RESULT 10
US-10-475-989-2
; Sequence 2, Application US/10475989
; Publication No. US20040142320A1
; GENERAL INFORMATION:
; APPLICANT: CNRS
; TITLE OF INVENTION: PROCESS FOR THE REPLICATION OF THE HEPATITIS C VIRUS
; FILE REFERENCE: WO/01 AA CNR GENO
; CURRENT APPLICATION NUMBER: US/10/475,989
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: FR 01/05732
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 9622
; TYPE: DNA
; ORGANISM: Hepatitis C virus
US-10-475-989-2

Alignment Scores:
Pred. No.: 4,22e-155 Length: 9622
Score: 1521.50 Matches: 263
Percent Similarity: 92.83% Conservativity: 9
Best Local Similarity: 89.76% Mismatches: 16
Query Match: 87.14% Indels: 5
DB: 18 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-10-475-989-2 (1-9622)
QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
DB 1461 GTGCTGCTCTATTTCGGCGCTC-----GACGCGGAACCCACGTCACC 1505
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
DB 1506 GGGGGAAGTCCGCGCACACACGCTGGGCTTGTGGTCTCTTACACAGCGGCAAG 1565
QY 51 GluAsnValGlnLeuLeuAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
DB 1566 CAGAAATCACTCACTGATCAACACACGCGAGTTGGCATCAATAGCAGCGCTTGAAC 1625
QY 71 CysAsnAspSerLeuAsnThrGlyTyrPheValGlyLeuPheThrHisLysPheAsn 90
DB 93.52% Conservativity: 11
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DB 1626 TGCACAGATAGCTTTACCACCGCTGGTTAGCAGGCTCTTCTATCGCCACAAAATTCAC 1685
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
DB 1686 TCTTCAGGCTGTCTCTGAGAGGTTGGCCAGCTGCCAGCGCTTACCGATTTGCCCCAGGGC 1745
QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
DB 1746 TGGGGTCCCATCATGTTATGCCAACGAGAGCGCTTGACGAACGCCCCCTACTCTGTGGCAC 1805
QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
DB 1806 TACCCTCCAAAGACCTTGTGGCATTTGTCCCGCAAGAGCGTGTGTGGCCGGTATATTGC 1865
QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
DB 1866 TTCACTCCACGCGCTGGTGTGGAAACGACGACAGCTCGGGCGGCTTACCTACGACG 1925
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
DB 1926 TGGGGTGCAAAATGATACGGATGCTTCGTCTTAACAACACACGCGCCACCGCTGGGCAAT 1985
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
DB 1986 TGGTTCCGTTGTACCTGGATGAACCTCACTGGATTACCAAAAGTGTGCGAGCGCCCT 2045
QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
DB 2046 TGTGTCATCGAGGGGTGGCAACAACACTTGTCTTGGCCACATGATTGCTTCCGCAAA 2105
QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
DB 2106 CATCGGAAGCCACATACTCTCGGTCCGCTCGGTCTGGATACACCCAGGTGCATG 2165
QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
DB 2166 GTCGACTACCGCTATAGGCTTTGGCACTATCTCTGTACTATCAATTACCATATTCAAA 2225
QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
DB 2226 GTCAGGATGTACGTGGAGGGTTCGAGCACAGCTGGAAGCGCCTGCAACTGGACGCG 2285
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
DB 2286 GCGGAACGCTGTGATCTGGAAGACAGGAGCAGGTCGAG 2324

RESULT 11
US-09-827-688-7
; Sequence 7, Application US/09827688
; Publication No. US20030165476A1
; GENERAL INFORMATION:
; APPLICANT: ORSON, FRANK
; APPLICANT: KINSEY, BERMA
; APPLICANT: BHOGAL, BALBIR
; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: P01949US1/10004014
; CURRENT APPLICATION NUMBER: US/09/827,688
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,680
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 9365
; TYPE: DNA
; ORGANISM: HEPATITIS C
US-09-827-688-7

Alignment Scores:
Pred. No.: 8,68e-155 Length: 9365
Score: 1518.50 Matches: 263
Percent Similarity: 93.52% Conservativity: 11
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Best Local Similarity: 89.76% Mismatches: 14
Query Match: 86.97% Indels: 5
DB: 10 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-09-827-688-7 (1-9365)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
DB 1449 GTGCTGCTGCTATTGCGCGGTT-----GACGCGGAACCCACGTCACC 1493

QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
DB 1494 GGGGGAAGTCCGCGCCACACACGCGTGGCTGTTCCTCTCCCTTTCCAGCGCGCAAG 1553

QY 51 GlnAsnValGlnLeuLeuLeuAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
DB 1554 CAGNACATCCACTGATCAACACACGCGGAGTTGGCACATCAATAGCAGCGCTTGAAC 1613

QY 71 CysAsnAspSerLeuLeuLeuThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90
DB 1614 TGCATGAAGACCTTAACACCGGCTGGTTAGCAGGCTCTTCTATCACCACAAATTCAC 1673

QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
DB 1674 TCTTCAGTGTCTCTGAGAGGTTGGCCAGCTGCGGACGCTTACCGGATTTTGCCCAAGGC 1733

QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
DB 1734 GGGGTCCTATCAGTACGCGCAACGCGGAGCGCTCGATGAAAGCGCCCTACTCTGGCAC 1793

QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
DB 1794 TACCTCTCAAGACCTTGTGGCATTTGTCCCGCAAGAGCGTGTGTGGCCGGTATATTC 1853

QY 151 PheThrProSerProValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
DB 1854 TTCACCTCCAGCCCCGTTGGTGGGAACACGACAGGTGGGCGCGCTACTCTACAGC 1913

QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnThrArgProProLeuGlyAsn 190
DB 1914 TGGGTCGCAATGATACGGATGCTTTGTCTTCTTAACACACGCGCCACGCTGGGCAAT 1973

QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
DB 1974 TGGTTCGGTTGCACTTGGATGAATCACTGATGATTCACCAAGTGTGGGAGCGCCCT 2033

QY 211 CysValIleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
DB 2034 TGTGTATCGAGGGGGTGGGCAACACACCTTGTCTGTCCCACTGATTTCCGCAAG 2093

QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
DB 2094 CATCCGGAACCACTACTCTCGGTGGGCTCGGTCCCTGGATTAACCCAGGTGATG 2153

QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
DB 2154 GTCGACTACCGGTATAGGCTTTGGCACTATCTTGTACCATCAATTAACCAATTCAAA 2213

QY 271 IleArgMetTyrValGlyGlyValGluHisArgLeuGluAlaLysCysAsnTrpThrArg 290
DB 2214 GTCAGATGTACGTGGAGGGGTCGAGCAGAGCTGGAGCGGCTGCAACTGGACGCGG 2273

QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
DB 2274 GCGCAAGCTGTGATCTGGNAGACAGGACAGGTCCGAG 2312

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RESULT 12

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US-09-238-076-1
; Sequence 1, Application US/09238076
; Patent No. US20020102540A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C

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```

; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/238,076
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/034,756
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9646 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-09-238-076-1

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Alignment Scores:
Pred. No.: 1,92e-154 Length: 9646
Score: 1515.50 Matches: 262
Percent Similarity: 92.83% Conservative: 10
Best Local Similarity: 89.42% Mismatches: 16
Query Match: 86.80% Indels: 5
DB: 9 Gaps: 1

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US-10-715-665-7_COPY_1_303 (1-303) x US-09-238-076-1 (1-9646)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
DB 1461 GTGCTGCTGCTATTGCGCGGCTC-----GACGCGGAACCCACGTCACC 1505

QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
DB 1506 GGGGGAAGTCCGCGCCACACGCGTGGCTGTTCCTTACACGAGCGCAAG 1565

QY 51 GlnAsnValGlnLeuLeuLeuAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
DB 1566 CAGAACATCAACTGATCAACACCAACGCGGAGTTGGCACATCAATAGCAGCGCTTGAAC 1625

QY 71 CysAsnAspSerLeuLeuLeuThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90
DB 1626 TGCATGAAGACCTTAACACCGGCTGGTTAGCAGGCTCTTCTATCAGCACAATTCAC 1685

QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
DB 1686 TCTTCAGGCTGTCTCAGAGGTTGGCCAGCTGCGGACGCTTACCGATTTTGCCAGGC 1745

QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
DB 1746 TGGGGTCTCTATCAGTTATGCCAACGGAAGCGGCTCGACGAGACGCCCTACTCTGTGCAC 1805

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QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 1806 TACCCTCCAAGACCTTGTGGCATTGTGCCGGAAGAGCGTGTGGCCCGGTATATTGC 1865
QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 1866 TTCACTCCCGAGCCCGTGGTGGTGGGAACACGACAGGTGGGGCGCGCTACCTACAGC 1925
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1926 TGGGGTGCAATGATACGGATGCTTCGTCTTAAACAACACAGGCCACCGCTGGGCAAT 1985
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 1986 TGGTTCGGTGTACCTGGATGAACCTCACTGGATTACCAAAAGTGTGGGAGCGCCCT 2045
QY 211 CysValIleGlyValAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 2046 TGTGTCATCGAGGGGTGGGCAACACACTTGTCTGCGCCCACTGATTGTTTCGCAAG 2105
QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 2106 CATCGGAAGCCACATACCTCTCGGTGGGCTCCGGTCCCTGGATTACACCCAGGTGCATG 2165
QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 2166 GTCGACTACCCGCTATAGGCTTTGGCAGTATCTCTGTACCATCAATTACACCATATTCAA 2225
QY 271 IleArgMetTyrValGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
Db 2226 GTCAAGATGTAGTGGAGGGGTGCAGCACAGGTGGAGCGGCTGCACCTGGACGCG 2285
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303
Db 2286 GCGAAGCGTGTGATCTGGAAGACAGGACAGGTCCGAG 2324
```

RESULT 13

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US-09-995-937-1
; Sequence 1, Application US/09995937
; Publication No. US20030028010A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,937
; FILING DATE: 28-No. US20030028010A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,756
; FILING DATE: 04-May-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 9646 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-937-1

Alignment Scores:
Pred. No.: 1,92e-154 Length: 9646
Score: 1515.50 Matches: 262
Percent Similarity: 92.83% Conservative: 10
Best local Similarity: 89.42% Mismatches: 16
Query Match: 86.80% Indels: 5
DB: 10 Gaps: 1

US-10-715-665-7_COPY_1_303 (1-303) x US-09-995-937-1 (1-9646)

QY 11 ValLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30
Db 1461 GTGCTGTGCTGCTATTTTGGCGGGCTC-----GACGCGGAACCCACGCTCACC 1505
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50
Db 1506 GGGGAAGTGGCGGCGGACACAGGCTGGGCTTGTGTGCTCTCTTACACAGGCGGCAAG 1565
QY 51 GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn 70
Db 1566 CAGAACATCCAACTCATCAACACCAACAGCGAGTTGGCACATCAATAGCAGCGCTTGAAC 1625
QY 71 CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisHisLysPheAsn 90
Db 1626 TGCAATGAAGCCTTAAACACCGGCTGGTTAGCAGGCTCTTCTATCAGCACAAATTTCAAC 1685
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110
Db 1686 TCTTCAGGCTGTCTTGAGAGGTGGCCAGCTGCCAGCGCTTACCGATTTTCCCGCAGGCG 1745
QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130
Db 1746 TGGGGTCTCTATCAGTTATGCCAACGGAAGCGGCTCGACGAACGCGCTTACTGTCTGGCAC 1805
QY 131 TyrProProLysProCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150
Db 1806 TACCCTCCAAGACCTTGTGGCATTGTGCCGGAAGAGCGTGTGGCCCGGTATATTGC 1865
QY 151 PheThrProSerProValValValGlyThrThrAspArgSerGlyAlaProThrTyrSer 170
Db 1866 TTCCTCCAGCCCGTGGTGGTGGGAACACGACAGGTCCGGCGGCGCTACCTACAGC 1925
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190
Db 1926 TGGGGTGCAATGATACGGATGCTTCGTCTTAAACAACACAGGCCACCGCTGGGCAAT 1985
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210
Db 1986 TGGTTCGGTGTACCTGGATGAACCTCACTGGATTACCAAAAGTGTGGGAGCGCCCT 2045
QY 211 CysValIleGlyValAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLys 230
Db 2046 TGTGTCATCGAGGGGTGGGCAACACACTTGTCTGCGCCCACTGATTGTTTCGCAAG 2105
QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250
Db 2106 CATCGGAAGCCACATACCTCTCGGTGGGCTCCGGTCCCTGGATTACACCCAGGTGCATG 2165
QY 251 ValAspTyrProTyrArgLeuTrpHisTyrProCysThrIleAsnTyrThrIlePheLys 270
Db 2166 GTCGACTACCCGCTATAGGCTTTGGCAGTATCTCTGTACCATCAATTACACCATATTCAA 2225
QY 271 IleArgMetTyrValGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290
```

Db 2226 GTCCAGGATGACGTGGAGGGTCCAGCACAGGCTGCAACTGGACGGG 2285  
QY 291 GlyGluArgCysAspLeuGluAspAlaAspArgSerGlu 303  
Db 2286 GCGGACGCTGTGATCTGGAGACAGGACAGGTCCGAG 2324

## RESULT 14

US-09-917-563-1  
; Sequence 1, Application US/09917563  
; Publication No. US20030073080A1  
; GENERAL INFORMATION:

; APPLICANT: RICE, CHARLES et al.  
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C  
; VIRUS (HCV) AND USES THEREOF

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOWELL & HAFERKAMP, L.C.

; STREET: 7733 FORSYTH BLVD., SUITE 1400

; CITY: ST. LOUIS

; STATE: MO

; COUNTRY: USA

; ZIP: 63105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/917,563

; FILING DATE: 27-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/238,076

; FILING DATE: 26-JAN-1999

; ATTORNEY/AGENT INFORMATION:

; NAME: HOLLAND, DONALD R.

; REGISTRATION NUMBER: 35,197

; REFERENCE/DOCKET NUMBER: 6029-4831

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 314-727-5188

; TELEFAX: 314-727-6092

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9646 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

## US-09-917-563-1

Alignment Scores:  
Pred. No.: 1.92e-154 Length: 9646  
Score: 1515.50 Matches: 262  
Percent Similarity: 92.83% Conservative: 10  
Best Local Similarity: 89.42% Mismatches: 16  
Query Match: 86.80% Indels: 5  
DB: 10 Gaps: 1

US-10-715-665-7\_COPY\_1\_303 (1-303) x US-09-917-563-1 (1-9646)

QY 11 valLeuLeuLeuCysGlyAlaValPheValSerProSerAlaSerGluThrHisValThr 30  
Db 1461 GTCTGCTGCTATTTCGCCGCTC-----GACCGGAAACCCACGTCACC 1505  
QY 31 GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaLys 50  
Db 1506 GGGGGGAAGTCCCGCCGACACAGGCTGGGCTTTGGTCTCTTACACAGCGGCGAAG 1565  
QY 51 GlnAsnValGlnLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 70

Db 1566 CAGAACATCACTGATCAACACCAACGGCAGTTGGCACATCAATAGCAGCGCTTCAAC 1625  
QY 71 CysAsnAspSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 90  
Db 1626 TGAATGAAAGCCCTTAACACCGGCTGTTAGCAGGGCTCTTCTATCAGCACAAATTCAC 1685  
QY 91 SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly 110  
Db 1686 TCTTCAGGCTGTCTGAGAGGTTGGCCAGCTGCCAGCGCTTACCGATTGTCAGGCGC 1745  
QY 111 TrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHis 130  
Db 1746 TGGGGTCTCTATCAGTTATGCAACGGAAGCGGCTCGACGAAACGCCCTACTGCTGCAC 1805  
QY 131 TyrProProIleSerCysGlyIleValProAlaLysSerValCysGlyProValTyrCys 150  
Db 1806 TACCTCCAAAGCCTTGTGGCATTTGTCCCGCAAGAGCGTGTGTGCCCGGTATATTCG 1865  
QY 151 PheThrProSerProValValValValValValValValValValValValValVal 170  
Db 1866 TTCCTCCAGCGCCCGTGTGGTGGGACACGACAGGTTCGGGCGGCGCTACCTACAGC 1925  
QY 171 TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn 190  
Db 1926 TGGGGTGCATAATGATACGGATGTCTTCGTCTTAAACAAACACAGGCGCCACGCTGGCAAT 1985  
QY 191 TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProPro 210  
Db 1986 TGGTTCCGTTGTACCTGGATGAACTCACTGGGATTTCACCAAGGTGCGGAGCGGCCCT 2045  
QY 211 CysValIleGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAla 230  
Db 2046 TGTGTCTATCGAGGGGTGGGCAACACACTTGTCTGCCCGCCTGATTGTTCCGCAAG 2105  
QY 231 HisProAspAlaThrTyrSerArgCysGlySerGlyProTrpIleThrProArgCysLeu 250  
Db 2106 CATCCGGAAGCCACATACCTCTCGGTGCGGCTCGGTCCTCGGATTACACCGAGTGCATG 2165  
QY 251 ValAspTyrProTyrArgLeuThrHisTyrProCysThrIleAsnTyrThrIlePheLys 270  
Db 2166 GTCGACTACCCGTATAGGCTTTGGCACTATCTCTGTACCATCAATATACCATATTTCAA 2225  
QY 271 IleArgMetTyrValGlyValGluHisArgLeuGluAlaAlaCysAsnTrpThrArg 290  
Db 2226 GTCAGGATGTACGTGGAGGGGTGAGACAGGCTGGAAGCGGCTGCACTGGACCGG 2285  
QY 291 GlyGluArgCysAspLeuGluAspArgAspArgSerGlu 303  
Db 2286 GCGGAACGCTGTGATCTGGAAGACAGGACAGGTCGAG 2324

## RESULT 15

US-09-238-076-5  
; Sequence 5, Application US/09238076  
; Patent No. US20020102540A1  
; GENERAL INFORMATION:

; APPLICANT: RICE, CHARLES et al.

; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOWELL & HAFERKAMP, L.C.

; STREET: 7733 FORSYTH BLVD., SUITE 1400

; CITY: ST. LOUIS

; STATE: MO

; COUNTRY: USA

; ZIP: 63105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

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, APPLICATION NUMBER: US/09/238,076
, FILING DATE:
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: US 09/034,756
, FILING DATE:
, ATTORNEY/AGENT INFORMATION:
, NAME: HOLLAND, DONALD R.
, REGISTRATION NUMBER: 35,197
, REFERENCE/DOCKET NUMBER: 6029-48311
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 314-727-5188
, TELEFAX: 314-727-6092
, INFORMATION FOR SEQ ID NO: 5:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 12980 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: double
, TOPOLOGY: linear
, MOLECULE TYPE: CDNA
, HYPOTHETICAL: NO
, ANTI-SENSE: NO
US-09-238-076-5

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Alignment Scores:			
Pred. No.:	2,82e-154	Length:	12980
Score:	1515.50	Matches:	262
Percent Similarity:	92.83%	Conservative:	10
Best Local Similarity:	89.42%	Mismatches:	16
Query Match:	86.80%	Indels:	5
DB:	9	Gaps:	1

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Db	1461	GTGCTGTGTATTGGCGCGTC-----GACGCGAAACCCACGTCACC	1505
Qy	31	GlyGlySerAlaGlyHisThrValSerGlyPheValSerLeuLeuAlaProGlyAlaIys	50
Db	1506	GGGGGAAGTGGCGGCGCCACACGGCTGGGCTTGTGGTCTCTCTTACACAGCGGCGAAG	1565
Qy	51	GlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAlaLeuAsn	70
Db	1566	CAGAACATCCAACCTGATCAACACACCGCAGTTGGCACATCAATAGCAGCGCTTGAAC	1625
Qy	71	CysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTrpHisHisIysPheAsn	90
Db	1626	TGCAATGAAAGCCCTAAACACGGCTGGTTAGCAGGGCTCTTCTATCAGCACAAATTCAC	1685
Qy	91	SerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAspGlnGly	110
Db	1686	TCITTCAGCGTGTCTGTAGAGGTTGGCCAGCTGGCCGACGCTTACCGAATTTGGCCAGGGC	1745
Qy	111	TrpGlyProIleSerTrpAlaAsnGlySerGlyProAspGlnArgProTrpCysTrpHis	130
Db	1746	TGGGGTCTCTACGTTATGCCACGGAAGCGGCTTCGACGACGCCCTACTTCTGGCAC	1805
Qy	131	TyrProProIysProCysGlyIleValProAlaIysSerValCysGlyProValTyrCys	150
Db	1806	TACCTCCAGACCTTGTGGCATTTGTGCCGAAAGACGCTGTGTGCCCGGTATATTGC	1865
Qy	151	PheThrProSerProValvalGlyThrThrAspArgSerGlyAlaProThrTrpSer	170
Db	1866	TTCACTCCACGCCCGTGGTGGGAAACGACCGACAGGTGGGCGCGCTACTCTACAGC	1925
Qy	171	TrpGlyGluAsnAspThrAspValPheValLeuAsnAsnThrArgProProLeuGlyAsn	190
Db	1926	TGGGGTGCAATGATACGGATGTCTTCGTCTTAAACAACACGAGCCACCGCTGGGCAAT	1985
Qy	191	TrpPheGlyCysThrTrpMetAsnSerThrGlyPheThrIysValCysGlyAlaProPro	210
Db	1986	TGGTTGGGTGTACTGGATGAATCAACTGGAATTCACCAAGTGTGGGAGCGGCCCT	2045



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 15, 2005, 04:37:38 ; Search time 3682 Seconds  
(without alignments)

3132.394 Million cell updates/sec

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Perfect score: 1746

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-NSR=US10715665 @CGN 1 1 3437 @runat\_13042005\_165823\_28155 -NCFU=6 -ICPU=3  
-USER=US10715665 -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	9.8	899	2	BE277041
2	164	9.4	904	5	B0850108
3	159.5	9.1	716	2	BE408331
4	159.5	9.1	835	4	BG281371
5	157.5	9.0	761	4	BI771956
6	157	9.0	899	5	B0890669
7	157	9.0	913	4	BG476931
8	154.5	8.8	798	4	BG281523
9	154.5	8.8	1041	5	BQ072488

10	154	8.8	511	2	BE389162
11	153	8.8	1050	2	BE312788
12	153	8.8	1124	4	BM553317
13	150.5	8.6	860	5	BQ682920
14	150.5	8.6	893	6	CB992325
15	150	8.6	951	5	BQ687808
16	148.5	8.5	898	4	BI757143
17	148.5	8.5	969	1	AL550289
18	147.5	8.4	897	2	BF311265
19	147	8.4	904	5	BU157553
20	146.5	8.4	877	1	AU131845
21	146	8.4	967	5	BX449214
22	146	8.4	1034	2	BE314639
23	145.5	8.3	694	1	AL524377
24	145.5	8.3	942	5	BQ880098
25	144.5	8.3	797	7	CF994970
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30	143	8.2	1174	4	BG253421
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34	142	8.1	888	5	BQ689818
35	141.5	8.1	874	4	BG334653
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37	141.5	8.1	952	5	BU838355
38	141	8.1	943	4	BM804838
39	140.5	8.0	646	4	BG477928
40	140.5	8.0	711	4	BG476511
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45	140	8.0	845	5	BQ877849

ALIGNMENTS

RESULT 1  
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LOCUS 601178928F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3543990 5',  
DEFINITION mRNA sequence.  
ACCESSION BE277041  
VERSION BE277041  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 899)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLC238 row: h column: 07  
High quality sequence stop: 688.

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1. .899  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3543990"  
/tissue\_type="melanotic melanoma"



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QY 30 -----ThrGlyGlySerAlaGlyHisThrVal-----SerGly 40
Db 197 TGCAGCGAGCAAGGTGTTTCAACGGGGGCACCTGCCAGCAGGCCCTGTACTTCTCAGAT 256
QY 41 PheValSerLeuLeuAlaProGlyAlaLysGlnAsnVal-----53
Db 257 TTCGTGTGCAGTGCCTCCGGAAGGATTGCTGGGAAGTCTGTGTAATPAGATACCGAGGCC 316
QY 54 -----GlnLeuLeuAsnThrAsnGlySerTrpHisLeuAsnSerThrAla 68
Db 317 ACGTGTCTACGAGNACGAGGCATCAGTACAGGGCAGCTGGAGCAGCGGAGAGTGGC 376
QY 69 LeuAsnCysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisLys 88
Db 377 GCCGAGTGC-----ACCAACTGG-----394
QY 89 PheAsnSerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAsp 108
Db 395 ---AACAGCAGCGGTTGGCCCAAGCCCTACAGCGGGGGGAGGCCAGCCATCAGG 451
QY 109 GlnGlyTrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCys 128
Db 452 CTGGCCCTGGGAACCACTACTCGAGAAACCCAGATCGAGACTCAAAAGCCCTGTGTC 511
QY 129 Trp-----HisTyrProProLysProCysGlyIleValProAla-----141
Db 512 TACGTCTTTAAGCGGGGAAGTACAGCTCAGAGTTCTGCAGC---ACCCCTGCTGCTCT 568
QY 142 -----LysSerValCys-----GlyProValTyrCysPheThrProSerPro 155
Db 569 GAGGGAACAGTGACTGCTACTTTGGGAATGGGTGAGCCTTACCGTGACACGACAGC---625
QY 156 ValValValGlyThrThrAspArgSerGlyValAlaProThrTyrSerTrpGlyGluAsnAsp 175
Db 626 -----CTCACCAGTGGGTGCTCTGCTGCTCCCGTGGGAATTC-CATGAT 669
QY 176 ThrAspValPheValLeuAsnAsnThrArgProProLeu-----188
Db 670 CCTGATAGGCAAGGTTTACACAGCACAGAACCCAGTCGCCCCAGCAGTGGCGCTGGGCAA 729
QY 189 -----GlyAsnTrpPheGlyCysThrTrpMet-----197
Db 730 ACATAATTACTCGCGGATCCTGATGGGATGCCAAGCCCTGTGGCCACGTGCTGAAGAA 789
QY 198 ---AsnSerThrGlyPheThrLysVal-CysGlyAlaProProCysValIleGlyAl 216
Db 790 CCGCAAGTCACGTGGGATGACGGTATGTCCTCT-----GCTCCANCTGC 840
QY 216 aGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHisProAspAlaThrTy 236
Db 841 GGGCCTGAAGACAGTA-----CAGCCCAAGCCTCAGTTT 873
QY 236 r---SerArgCysGlySerGlyPro 243
Db 874 CGCATCAAAAGAGGGCTCTTCGCCG 898

RESULT 3
LOCUS BE408331 716 bp mRNA linear EST 21-JUL-2000
DEFINITION 601302704F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637273 5',
mRNA sequence.
ACCESSION BE408331
VERSION BE408331.1 GI:9344880
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 716)
TITLE NIH-MGC http://mgi.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

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Email: cgabs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLM336 row: g column: 02
High quality sequence start: 2
High quality sequence stop: 632.
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:3637273"
            /tissue_type="choriocarcinoma"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH MGC 21"
            /notes="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
            Site 2: EcoRI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCAGAG(G). Size-selected >500bp
            for average insert size 1.8kb. Library constructed by
            Ling Hong in the laboratory of Gerald M. Rubin (University
            of California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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## ORIGIN

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Alignment Scores:
Pred. No.: 0.0008 Length: 716
Score: 159.50 Matches: 69
Percent Similarity: 35.04% Conservative: 13
Best Local Similarity: 29.49% Mismatches: 93
Query Match: 9.14% Indels: 59
DB: 2 Gaps: 13

US-10-715-665-7_COPY_1_303 (1-303) x BE408331 (1-716)

QY 1 MetAspAlaMetLysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal 20
Db 66 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 125
QY 21 SerProSerAlaSerGluThrHisVal-----ThrGlyGlySerAlaGlyHisThrVal 38
Db 126 TCGCCCGCAGC---CAGGAATCCATGCCCGCATTCAGAGAGGAGCCAGATCTTACCAAGTG 182
QY 39 -----SerGlyPheValSerLeuLeuAlaPro 47
Db 183 ATCTGCAGAGATGAAAAAACCAGCATGATATACCAGCAACATCATGCTGCTGCGCCCT 242
QY 48 GlyAlaLysGlnAsnValGlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThr 67
Db 243 GTGCTCAGAAAGCAAC-----CGGGTGGAAATATTGCTGG---TGCAACAGTGGC 287
QY 68 AlaLeuAsnCysAsnAsp-----SerLeuAsnThr 77
Db 288 AGGGCAGTGGCCACTCAGTCTGTCTCAAAAGTTGCAGCGCAGCAAGGTGTTTCACGGG 347
QY 78 GlyTrpLeuAlaGlyLeuPheTyrHisLysPheAsnSerSerGlyCysProGluArg 97
Db 348 GGCACCTGCAGCAGCGCCCTGACTTCTCAGATTTCGTGTGCCAG---TGCCCGGAAGGA 404
QY 98 LeuAla---SerCysArgProLeuThrAspPheAspGlnGlyTrpGlyProIleSerTyr 116
Db 405 TTTGTGGGAAGTGTGTGTAATAGATACAGGCCAGCTGTACGAGGACCAAGGATCA 464
QY 117 AlaAsnGlySerGlyProAspGlnArgProTyrCysTrpHisTyrProLysProCys 136
Db 465 GCTACAGGGGCGCTGGAGCACAGCGGAGAGTGGCG-----CGAGTGACCAACT 515
QY 137 GlyIleValProAlaLysSerValCysGlyProValTyrCysPheThrProSerProVal 156
Db 137 GlyIleValProAlaLysSerValCysGlyProValTyrCysPheThrProSerProVal 156

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Db      516 GGAACAGACGCGGT-----TGGCCAGAGACCCCTACA 548
QY      157 ValValGlyThrThraAspArgSerGlyAlaProThrTyrSerTrpGlyGluAsnAspThr 176
Db      549 GCGGGCGGAGCCAGACGCCATCAGC-----TGGCGCTGGGAACCACTACT 599
QY      177 AspVal-----PheValLeuAsnAsnThrArgPro 186
Db      600 GAGAAACACAGATCGAGACTCAAGCCTGGTGTCTACGTTTAAAGCGGGGAATACACGTCCA 659
QY      187 -----ProLeuGlyAsnTrpPheGlyCysThrTrpMet 197
Db      660 AGTTCGAACCCCTGCTGTCTTGGGACGCGTCTGTGGGATG 701

RESULT 4
LOCUS   BG281371
DEFINITION BG281371 835 bp mRNA linear EST 21-FEB-2001
          602401866F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4544200 5',
          mRNA sequence.
ACCESSION BG281371.1 GI:13030296
VERSION   BG281371
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 835)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC/DCMP/DTF
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: Image.llnl.gov
          Plate: LNCM1227 row: c column: 17
          High quality sequence stop: 826.

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                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_20"
                /notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5',
                adaptor: GGACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Alignment Scores:
Pred. No.: 0.000998 Length: 835
Score: 159.50 Matches: 68
Percent Similarity: 36.84% Conservative: 16
Best Local Similarity: 29.82% Mismatches: 86
Query Match: 9.14% Indels: 59
DB: 4 Gaps: 10

US-10-715-665-7_COPY_1_303 (1-303) x BG281371 (1-835)

QY      1 MetAspAlaMetIysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal 20
Db      84 ATGATGCAATGAAGAGGGCTCTGCTGTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 143

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QY      21 SerProSerAlaSerGluThrHisVal----- 29
Db      144 TCGCCACAGC-----CAGGAATCATGTCCTCCGATTCAGAGAGAGAGCCAGATCTTTACCAAGT 200
QY      30 -----ThrGlyGlySerAlaGlyHisThrVal-----SerGly 40
Db      201 TGCACGAGCCCAAGGTGTTTCAACGGGGGCACCTGCCAGCAGCGCCCTGTACTTCTCAGAT 260
QY      41 PheValSerLeuLeuAlaProGlyAlaLysGlnAsnVal----- 53
Db      261 TTCTGTGTCCAGATGCCCGAAGGATTTCTCTGGGAAGTCTCTGTAATAGATACCAAGGGCC 320
QY      54 -----GlnLeuIleAsnThrAsnGlySerTrpHisLeuAsnSerThrAla 68
Db      321 ACGTCTACGAGGACCGGCATCAGCTACAGGGGCACGTGGAGCAGCAGCGGAGAGTGGC 380
QY      69 LeuAsnCysAsnAspSerLeuAsnThrGlyTrpLeuAlaGlyLeuPheTyrHisLys 88
Db      381 GCCGAGTGC-----ACCAACTGG----- 398
QY      89 PheAsnSerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAsp 108
Db      399 ---AAACAGCAGCGCGTGTGGCCAGAAAGCCCTACAGCGGGCGGAGCCAGACCCATCAGG 455
QY      109 GlnGlyTrpGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCys 128
Db      456 CTGGGCGCTGGGAACACACAGATACATGTCAGAAACCCAGATCGAGATCAAGAGCCTGGTGC 515
QY      129 Trp-----HisTyrProProIysProCysGlyIleValProAlaLysSer 143
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QY      144 ValCysGlyProValTyrCysPheThrProSerProValValGlyThrThrAspArg 163
Db      573 GAG---GGAACACAGTGAAGTCTTCTGGGAATGGGTGAGTCCAGCTACCGTGGCAGCAGCAGG 629
QY      164 -----SerGlyAlaProThrTyrSerTrpGlyGluAsnAspThrAspValPheVal 180
Db      630 CTCACCGAGTGGGTGCTCTCTGCTCCGTTGGGAATTC-CATGATCTGTATAGGCAAGT 688
QY      181 LeuAsnAsnThrArgProLeu 188
Db      689 TTACACAGCAGCAAGAACCCAGTTG 712

BI771956 761 bp mRNA linear EST 25-SEP-2001
603058981F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5208117 5',
mRNA sequence.
ACCESSION BI771956.1 GI:15763534
VERSION   BI771956
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 761)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L14M1522 row: b column: 22
          High quality sequence stop: 738.
          Location/Qualifiers
            1..761
                source

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|::|
QY 142 ----LysSerValCys-----GlyProValTyr----- 149
|::|
576 GGGAAACAGTACTGCTTGGGAATGGGTCAAGCCTCAGCGTGGAGCGACAGGCTCAC 635
|::|
QY 150 -----CysPheThrProSerProValValValGlyThrThrAspArgse 164
|::|
636 GAAGTCGGGTGCTCTGTC-----TCCCGGGGATTCCTTGATCTCGGATACGGCA 686
|::|
QY 164 rGlyAlaPro-----ThrTyrSerTyrPbGlyGluAsnAs 175
|::|
687 AGGTACACCAACAGAACAGAACCCAGTGGCCAGGCACTGGGGCCTGGGCAAC----- 741
|::|
QY 175 pThrAspValPheValLeuAsnThrArgProProLeuGlyAsn-----TrpPh 192
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742 -----ATAATCACTGCCCGGAATCCTTGATGGGATGCCAAGCCCTGGGT 785
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QY 192 e---GlyCys-----ThrTyrMetAsnSerThrGlyPheThrLysVa 205
|::|
786 GCCCAGTTGCTGAAGAAACCGCAGGCTGACGTGG-----GAGTA 824
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QY 205 lCysGlyAlaProProCys 211
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825 CTGTGATGTGCCCTCTGT 843
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RESULT 8
BG281523 798 bp mRNA linear EST 21-FEB-2001
LOCUS 602402058F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4544223 5',
DEFINITION mRNA sequence.
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ACCESSION BG281523

VERSION 1 GI:13030448

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: ATCC/DCTD/BTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Plate: L1CWI227 row: d column: 16

High quality sequence stop: 794.

Location/Qualifiers

1..798

FEATURES

source

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="IMAGE:4544223"

/tissue\_type="melanotic melanoma"

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/clone\_lib="NIH MGC 20"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGACACAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

# Alignment Scores:

Pred. No.: 0.00261 Length: 798  
Score: 154.50 Matches: 65  
Percent Similarity: 30.31% Conservative: 12  
Best Local Similarity: 25.59% Mismatches: 75  
Query Match: 8.85% Indels: 103  
DB: 4 Gaps: 10

US-10-715-665-7\_COPY\_1\_303 (1-303) x BG281523 (1-798)

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84 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 143
|::|
QY 21 SerProSerAlaSerGluThrHisVal----- 29
|::|
144 TCGCCCCAGC---CAGGAATCCATGCCGATTCAGAAGAGGAGCCAGATCTTACCAAGGT 200
|::|
QY 30 -----ThrGlyGlySerAlaGlyHisThrVal-----SerGly 40
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201 TGCAGCGAGCCAAAGTGTTCACAGGGGGCACCTGCCAGCAGGCGCTGTACTTCTCAGAT 260
|::|
QY 41 PheValSerLeuLeuAlaProGlyAlaLysGlnAsnVal----- 53
|::|
261 TTCGTGTGCCAGTGGCCCCGAAAGGATTGGCTGGGAAGTGTGTGAAATAGATACACGGGCC 320
|::|
QY 54 -----GlnLeuIleAsnThrAsnGlySerTyrHisLeuAsnSerThrAla 68
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321 ACGTGTCTACGAGGACGAGCG-ATCAGCTACAGGGGCGACGTGGAGACAGCGGAGAGTGGC 379
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QY 69 LeuAsnCysAsnAspSerLeuAsnThrGlyTyrLeuAlaGlyLeuPheTyrHisHisLys 88
|::|
380 GCGCAGTGC-----ACCAACTGG----- 397
|::|
QY 89 PheAsnSerSerGlyCysProGluArgLeuAlaSerCysArgProLeuThrAspPheAsp 108
|::|
398 ---AACAGCAGCGCGTGGCGGCCCTACAGCGGGCGGAGGAGGAGGAGGAGGAGGAGGAG 454
|::|
QY 109 GlnGlyTyrGlyProIleSerTyrAlaAsnGlySerGlyProAspGlnArgProTyrCys 128
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455 CTGGGCTGGGGAACCAACACTACTGCAGAAACCCAGATCGAGACTCAAAAGCCCTGTGTC 514
|::|
QY 128 ----- 128
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515 TAGCTCTTTAAGCGGGGAAGTACAGCTCAGAGTTCTCGAGGACCCCTGCGCTCTCTGA 574
|::|
QY 129 -----TrpHisTyrProProLys 134
|::|
575 GGGAAACAGTACTGCTACTTTGGGAATGGGTCAAGCTACCGTGGCAGCAGCAGCCTCAC 634
|::|
QY 135 ProCysGlyValProAlaLysSerValCysGlyProValTyrCysPheThrProSer 154
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635 CGAGTCGGG-----TGCCTCTGCGCT--- 655
|::|
QY 155 ProValValValGlyThrThrAspArgSerGly-----AlaPro 167
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656 CCGGTGGGAATTCATGATCTCTGATAGGCAAGTTTACACAGCAGCAGACAGAGCCAGTCCCA 715
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QY 168 ThrTyrSerTyrGlyGluAsnAspThrAspValPheValLeu 181
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# RESULT 9

BQ072488

LOCUS BQ072488

DEFINITION

AGENCOURT\_6839035 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5761678

5', mRNA sequence.

ACCESSION BQ072488

VERSION BQ072488.1

KEYWORDS

SOURCE EST.

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;







QY	176	rAspValPheValLeuAsnAsnThrArgProProLeu-----GlyAsnTr	191
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QY	191	pPheGlyCysThrTrpMetAsnSerThrGlyPheThrLysValCysGlyAlaProProCy	211
DB	716	-TTTGGG---GATTGGGTGAGTACACCGGG---ACGCACAGCTCCCCCGAGTGGGTG	768
QY	211	sValleGlyGlyAlaGlyAsnAsnThrLeuHisCysProThrAspCysPheArgLysHi	231
DB	769	CCTCTGACTTCCCGGGGAATTCCCTGATACCTGTAGCGCAGCGGTTTTC-----	820
QY	231	sProAspAlaThrTrpSer-----	238
DB	821	-CCGGCGCGG---TATAGCCCCCGTCTCTCCGGCAGCTGGCTTGGCGCACCTATT	876
QY	238	CysGlySerGlyPro-----TrrPheThrProArg	248
DB	877	GATGGGGCGGACCGTACTGGGGTGGCTCACACCCCGT	916
RESULT 12			
LOCUS	BM553317	1124 bp mRNA linear EST 20-FEB-2002	
DEFINITION	AGENCY COURT 6542530 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742949		
ACCESSION	BM553317	5', mRNA sequence.	
VERSION	BM553317.1	GI:18791943	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaabs-r@mail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLAM12761 row: 0 column: 14		
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	/clone_lib="NIH_MGC_119"		
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	Site 2: EcoRV (destroyed); RNA source normal medulla from		
	anonymous male age 27. Library is oligo-dT primed and		
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	cloning). Average insert size 1.3 kb, insert size range		
	0.9-3 kb. Library is normalized and enriched for		
	full-length clones and was constructed by C. Gruber		
	(Invitrogen). Research Genetics tracking code 013. Note:		
	this is a NIH_MGC Library."		
ORIGIN			
Alignment Scores:			
Pred. No.:	0.00581	Length:	1124
Score:	153.00	Matches:	81
Percent Similarity:	30.23%	Conservative:	26
Best Local Similarity:	22.88%	Mismatches:	108
Query Match:	8.76%	Indels:	139

DB:	4	Gaps:	14
US-10-715-665-7_COPY_1_303 (1-303) x BM553317 (1-1124)			
QY	1	MetAspAlaMetLysArgGlyLeuCysCysValLeuLeuLeuCysGlyAlaValPheVal	20
DB	87	ATGGATCAATGAAGAGAGGGCTCTGCTGTGTGTCTGTCTGTGTGTGGAGCAGTCTCGT	146
QY	21	SerProSerAlaSerGluThrHisVal-----	29
DB	147	TCGCCAGC---CAGGAAATCCATGCGCGGATTTCAGAGAGGAGCCAGATCTTACCAAGTG	203
QY	29	-----	29
DB	204	ATCTGCAGAGATGAAAAAACCAGATGATATACAGCAACATCACTGCTGCGCCCT	263
QY	30	-----ThrGlyGlySerAlaGlyHis	36
DB	264	GTGCTCAGAGCAACCGGGTGAATATTGCTGGTCAACAGTGCAGGGCAGGCGCACAGTGCCAC	323
QY	37	ThrVal-----	38
DB	324	TCAGTGCCTGTCAAAAGTTGCAGCGAGCAAGGTGTTTCAACGGGGGCACCTGCCAGCAG	383
QY	39	-----SerGlyPheValSerLeuLeuAlaProGlyAlaLysGlnAsnVal---	53
DB	384	GCCCTGTACTTCTCAGATTTCGTGCCAGTGCCTCCCGAAGGATTGCTGGGAGTGTCTGT	443
QY	54	-----GlnLeuIleAsnThrAsnGlySerTrp	62
DB	444	GAAATAGATACCAGGGCCACGTGTCTACGAGGACACGAGGCATCAGCTACAGGGGCACGTGG	503
QY	63	HisLeuAsnSerThrAlaLeuAsnCysAsnAspSerLeuAsnThrGlyTrpLeuAlaGly	82
DB	504	AGCAGCGGAGAGTGGCGCCGAGTGC-----ACCACTGG-----	539
QY	83	LeuPheTyrHisHisLysPheAsnSerSerGlyCysProGluArgLeuAlaSerCysArg	102
DB	540	-----AACAGACGGGTGGCCAGAACCCCTACAGCGGGCGG	578
QY	103	ProLeuThrAspPheAspGlnGlyTrpGlyProIleSerTrpAlaAsnGlySerGlyPro	122
DB	579	AGGCAGATGCCATCAGCTGGCGCTGGGAAACCACTACTCTGAGAAACCCAGATCGA	638
QY	123	AspGlnArgProTyrCysTrp-----HisTyrProProLysProCysGly	137
DB	639	GACTCAAGCCCTGTGTCTACGTCTTTAAGCGGGGAAGTACAGCTCAGAGTTCTGCAGC	698
QY	138	Ile-ValProAlaLysSerValCysGlyProValTyrCysPheThrProSerProValVa	157
DB	699	ACCCCTGCTCTCTGAGGGAACAGTACTCTACTTTGGGAATGGGTACGCTACCTACCT	758
QY	157	lValGlyThrThrAspArgSerGlyAlaProThrTrpSerTrpGlyGluAsnAspThrAs	177
DB	759	GGCAGCACAGCTCACAGTCCGCTCTCTGCTCCCGTGAATTCATGATCCTGA	818
QY	177	pValPheValLeuAsnAsnThrArg-----ProProLeuGlyAsnTrpPhe-----	192
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QY	193	-----GlyCys---ThrTrp-----MetAsnSerTh	200
DB	879	AATTACTGCCGGGAATCTGTATGGGGGATCCAGCCCTGGTCCCGTGTCTGAGAACCC	938
QY	200	rglyPheThr-----LysValCysGlyAlaProProCysValIleGlyGlyAlaGlyAs	218
DB	939	AGGNCCTGACCTGGGAANTACTGTGATGTCCTCTCTGCTCCCTTGGGNC-----	990
QY	218	nAsnThrLeuHisCysProThrAspCysPheArgLysHisProAspAlaThrTyrSer--	237
DB	991	-----TTGAGCAGTACAGCCAGGCGCTCATTTTCCCA	1022
QY	238	-----ArgCysGlySerGlyPro	243

Db	258	GTGCTCAGAAGCAAC-----CGGTGGGAATATTGCTGG-----TGCACAGTGGC	302
Qy	68	AlaLeuAenCysAenAsp- 	77
Db	303	AGGCACAGTCCCACTCAGTGCCTGTCAAAAGTTGCAGCGAGCCAAAGTGTTCACCGG	362
Qy	78	GlyTrpLeuAlaGlyLeuPheTyRhiShiSlysPheAenSerSerGlyCysProGluArg	97
Db	363	GGCACCTGCCACAGCGCCCTGTACTCTTCAGATTTCGTGTGCCAG---TGCCCCGAAGGA	419
Qy	98	LeuAla- 	111
Db	420	TTTGCTGGGAAGTCTGTGAAATAGATACAGGCCACCTGCTACGAGACACAGGC---	476
Qy	112	GlyProIleSerTyAla- 	117
Db	477	-----ATCAGCTACAGGGGCACGTGGAGCAGCGGAGAGTGGCGCCGAGTGCACCAAC	530
Qy	118	---AsnGlySerGlyProAspGlnArgProTyRysTrpHisTyRProProllysProCys	136
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Qy	137	GlyIleValProAlaLysSerValCysGlyProValTyRysPheThrProSerProVal	156
Db	582	-----GCCATCAGCTGGCGCTGGGAGCCACCACTACTCGAGAAACCCA-	626
Qy	157	ValValGlyThrThrAspArgSerGlyAlaPro- 	168
Db	627	-----GATCGAGACTCAAGCCCTGGTGCTACGTCTTTAAGCGGNGAAG	671
Qy	169	TyrSerTrpGlyGluAenAspThrAspValPheValLeuAenAenThrArgProProLeu	188
Db	672	TACAGCTCAAAGTTCTCGAGCACCCCTGCCTCTGAGGAAACAGTGTACCTT	731
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DEFINITION	IMAGE:30237748 5', mRNA sequence.		
ACCESSION	CB992325		
VERSION	CB992325.1 GI:30286845		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 893)		
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapsb@remail.nih.gov Tissue Procurement: Dr. Stefan Hansson cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM363 row: e column: 21 High quality sequence stop: 409. Location/Qualifiers 1 .893 /organism="Homo sapiens"		
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
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Listing first 45 summaries

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- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	834.8	52.4	1207	6 AR004336	Sequence
5	834.8	52.4	1207	6 AR006827	Sequence
6	834.8	52.4	8316	6 AR118703	Sequence
7	834.8	52.4	9185	6 AR118722	Sequence
8	834.8	52.4	9185	6 AR118723	Sequence
9	834.8	52.4	9185	6 I08294	Sequence 1
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15	834.8	52.4	9401	6 I71894	Sequence 9
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ALIGNMENTS

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AX154501  
LOCUS AX154501 5882 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 6 from Patent WO0138358.  
ACCESSION AX154501  
VERSION AX154501.1 GI:14536111  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
AUTHORS Selby, M.C., Glazer, E.C. and Houghton, M.C.  
TITLE Hbv/hcv virus-like particle  
JOURNAL Patent: WO 0138358-A 6 31-MAY-2001;  
CHIRON CORPORATION (US)  
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 Intracellular production of hepatitis C E1 and E2 truncated polypeptides.  
 BD132859.1 GI:23227804  
 JP 2002504810-A/2.  
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 1 (bases 1 to 1989)  
 Houghton, M., Choo, Q.L., Abrignani, S., Chien, D., Selby, M. and Glazer, E.  
 Intracellular production of hepatitis C E1 and E2 truncated Patent: JP 2002504810-A 2 12-FEB-2002;  
 CHIRON CORP  
 OS Hepatitis virus (hepatitis C virus)  
 PN JP 2002504810-A/2  
 PD 12-FEB-2002  
 PF 06-MAY-1998 JP 1998548360  
 PR 06-MAY-1997 US 60/045675  
 PI MICHAEL HOUGHTON, QUI LIM CHOO, SERGIO ABRIGNANI, DAVID CHIEN, MARK SELBY, EDWARD GLAZER  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9185)  
AUTHORS Houghton, M., Choo, Q.-L., and Kuo, G.  
TITLE NABV diagnostics and vaccines  
JOURNAL Patent: EP 0388232-A1 1 19-SEP-1990;  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 9185)  
AUTHORS Weiner, A.J., Steimer, K.S. and Houghton, M.  
TITLE HCV cultivation method in eucaryotic cells  
JOURNAL Patent: JP 2001314192-A 3 13-NOV-2001;  
CHIRON CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001314192-A/3  
PD 13-NOV-2001  
PF 15-MAR-2001 JP 2001075114  
PI 25-AUG-1989 US 398667  
PR AMY J WEINER, KATHELYN S STEIMER, MICHAEL HOUGHTON PC  
C12N15/09, C12N5/10, C12N7/00// (C12N7/00, C12R1.93), C12N15/00, PC  
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DB 2020 TCCTGTGTATCGGAGGGCGGCAACACACCTGCACTGCCCACTGATTTGCTTCG 2079

QY 687 CAAAGCATCCGAGCGCCACATCTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTG 746  
DB 2080 CAAAGCATCCGAGCGCCACATCTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTG 2139

QY 747 CTTGCTGCACTACCCGTATAGGCTTTGGCATATCTCTGTACCATCACTACACCATATT 806  
DB 2140 CTTGCTGCACTACCCGTATAGGCTTTGGCATATCTCTGTACCATCACTACACCATATT 2199

QY 807 TAAATCAGGATCTAGTGGAGGGTGCACACAGGCTGGAGCTGCCTGCACCTGGAC 866  
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1840 TTGCTTCACTCCAGCCCCGTGGTGGGAACGACCGAGCTGGGGCGCCACACCTA 1899  
507 CAGCTGGGGTGAATATGATACGAGCGTCTTCGCTCTTAAACAATACGAGCCACCGCTGGG 566  
1900 CAGCTGGGGTGAATATGATACGAGCGTCTTCGCTCTTAAACAATACGAGCCACCGCTGGG 1959  
567 CAATTGGTTCCGTTGATCCTGATGAACTCAACTGATTCACCAAGTGTGCGGAGCGCC 626  
1960 CAATTGGTTCCGTTGATCCTGATGAACTCAACTGATTCACCAAGTGTGCGGAGCGCC 2019  
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2020 TCCTTTGTGTCATCGGAGGGCGGCAACAACACCTGCACTGCCCACTGATTGCTTCGG 2079  
687 CAAGCATCCGAGCGCCACATACTCTCGGTCCGGCTCCGGTCCCTGGATCACACCCAGGTG 746  
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747 CTGCTGCACTACCGGTATAGCTTTGGCAATTATCCTTTGATCATTCACTACCATATT 806  
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2260 GCGGGCGCAACGTTGCGATCTCGAAGATAGGACAGGTCGAGATC 2305

RESULT 11  
AR166930  
LOCUS AR166930 9379 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 1 from patent US 6284249.  
ACCESSION AR166930  
VERSION AR166930.1 GI:16243325  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9379)  
AUTHORS Barban,V.  
TITLE Fusion polypeptide having the C protein and E1 protein of hepatitis C virus  
JOURNAL Patent: US 6284249-A 1 04-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..9379  
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ORIGIN  
Query Match 52.4%; Score 834.8; DB 6; Length 9379;  
Best Local Similarity 96.4%; Pred. No. 3.3e-220;  
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
27 CTGTGTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCGCAGCGCTAGCGAAACCCACGT 86  
1420 CTGGGCGAAGTCTCTGTAGTGTCTGCTATTTCGCGCGCTCGACGCGGAAACCCACGT 1479  
87 CACCGGGGAAGTCCGCGGCACACTGTGTCTGGAATTTGATGCTCTCGACACGAGCGC 146  
1480 CACCGGGGAAGTCCGCGGCACACTGTGTCTGGAATTTGATGCTCTCGACACGAGCGC 1539  
147 CAAGCAGAAGCTCCAGCTGATCAACACAGGCGAGTTCGCACCTCAATAGCAGCGCCT 206  
1540 CAAGCAGAAGCTCCAGCTGATCAACACAGGCGAGTTCGCACCTCAATAGCAGCGCCT 1599  
207 GAACTGCAATGATAGCTCAACACCGGCTGGTTGGCAGGCGCTTTCTATCACCACAAGTT 266  
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267 CAATCTTTCAAGCTGTCTCTGAGAGCTAGCCAGCTGCGGACCCCTTACCATTGTTGACCA 326  
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1720 GGGCTGGGGCCCTATCAGTTATGCAACGGAAGGGGCCCCGACCAAGCGCCCTACTGCTG 1779  
387 GCATACACCCCAAAACCTTCGGGTATTGTCCCGCGGAAGAGTGTGTGTCGCGGTATA 446  
1780 GCATACACCCCAAAACCTTCGGGTATTGTCCCGCGGAAGAGTGTGTGTCGCGGTATA 1839  
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567 CAATTGGTTCCGTTGATCCTGATGAACTCAACTGATTCACCAAGTGTGCGGAGCGCC 626  
1960 CAATTGGTTCCGTTGATCCTGATGAACTCAACTGATTCACCAAGTGTGCGGAGCGCC 2019  
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2020 TCCTTTGTGTCATCGGAGGGCGGCAACAACACCTGCACTGCCCACTGATTGCTTCGG 2079  
687 CAAGCATCCGAGCGCCACATACTCTCGGTCCGGCTCCGGTCCCTGGATCACACCCAGGTG 746  
2080 CAAGCATCCGAGCGCCACATACTCTCGGTCCGGCTCCGGTCCCTGGATCACACCCAGGTG 2139  
747 CTGCTGCACTACCGGTATAGCTTTGGCAATTATCCTTTGATCATTCACTACCATATT 806  
2140 CTGCTGCACTACCGGTATAGCTTTGGCAATTATCCTTTGATCATTCACTACCATATT 2199  
807 TAAATACAGGATGACGTGGGAGGGTCGAACACAGGCTGGAAGCTGCCCTGCAACTGGAC 866  
2200 TAAATACAGGATGACGTGGGAGGGTCGAACACAGGCTGGAAGCTGCCCTGCAACTGGAC 2259  
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2260 GCGGGCGCAACGTTGCGATCTCGAAGATAGGACAGGTCGAGATC 2305

RESULT 12  
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LOCUS AR301300 9379 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 1 from patent US 6538123.  
ACCESSION AR301300  
VERSION AR301300.1 GI:31689076  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 9379)  
AUTHORS Barban,V.  
TITLE Vaccine composition for preventing or treating hepatitis C  
JOURNAL Patent: US 6538123-A 1 25-MAR-2003;  
FEATURES Location/Qualifiers  
source 1..9379  
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ORIGIN  
Query Match 52.4%; Score 834.8; DB 6; Length 9379;  
Best Local Similarity 96.4%; Pred. No. 3.3e-220;  
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
27 CTGTGTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCGCAGCGCTAGCGAAACCCACGT 86  
1420 CTGGGCGAAGTCTCTGTAGTGTCTGCTATTTCGCGCGCTCGACGCGGAAACCCACGT 1479

QY 87 CACCGGGGAAGTGC CGGCACACTGTGTCTGATTTGTTAGCTCTCGCACCGCGC 146  
Db CACCGGGGAAGTGC CGGCACACTGTGTCTGATTTGTTAGCTCTCGCACCGCGC 1539  
QY 147 CACGACAGAGCTCCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCAGGCCCT 206  
Db CACGACAGAGCTCCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCAGGCCCT 1599  
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QY 327 GGGCTGGGGCCCTATCAGTTATGCCAAACGAGCGGCCCGGACCGGCCCTTACTGCTG 386  
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QY 387 GCATCTACCCCCCAAAACCTTGCCTGATTTGTCGGGGAAGAGTGTGTGTCCGGTATA 446  
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QY 447 TTGCTTCACTCCAGCCCCGCTGTGTGGGAACGACGACAGTCGGCGCGGCCACCTA 506  
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QY 627 TCCTTGTGTATCGGAGGGCGGCAACCAACCCCTGCACTGCCCACTGATTGCTTCG 686  
Db TCCTTGTGTATCGGAGGGCGGCAACCAACCCCTGCACTGCCCACTGATTGCTTCG 2079  
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Db CACGATCCGAGCGGCACATCTCTGGTCCGGCTCCGCTCCCTGATCACACCCAGTG 2139  
QY 747 CTTGTCGACTACCCCTATAGCTTTGGCATTTATCTTGATCACTCAACTACACCATATT 806  
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RESULT 13  
LOCUS ARI176483 9401 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 9 from patent US 6312889.  
ACCESSION ARI176483  
VERSION ARI176483.1 GI:17918838

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 9401)  
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.  
TITLE Combinations of hepatitis c virus (HCV) antigens for use in  
immunassays for anti-HCV antibodies  
JOURNAL Patent: US 6312889-A 9 06-NOV-2001;  
FEATURES Location/Qualifiers

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Query Match 52.4%; Score 834.8; DB 6; Length 9401;  
Best Local Similarity 96.4%; Pred. No. 3.3e-220;  
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 27 CTGTGTGCTGCTGTGTGGAGCAGTCTTCGTCGCCACGCGCTAGCGAAACCCACG 86  
Db CTGGGCGAAGGCTCTGTGTAGTGTCTATTTGCGCGGCTGCGACGCGAAACCCACG 1501  
QY 87 CACCGGGGAAGTGC CGGCACACTGTGTCTGATTTGTTAGCTCTCGCACCGCGC 146  
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QY 147 CACGACAGAGCTCCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCAGGCCCT 206  
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RESULT 14  
LOCUS E66593 9401 bp DNA linear PAT 18-JUN-2001



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DEFINITION Hepatitis C virus asialoglycoprotein.
ACCESSION E66593
VERSION E66593.1 GI:13026028
KEYWORDS JP 1999071395-A/1.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Virus: ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepadnavirus.
REFERENCE 1 (bases 1 to 9401)
AUTHORS Robert,O.R., Frank,M., Kent,B.S., Barbara,A.J. and John,A.H.
TITLE Hepatitis C virus asialoglycoprotein
JOURNAL Patent: JP 1999071395-A 1 16-MAR-1999;
CHIRON CORP
COMMENT OS Hepatitis C virus
PN JP 1999071395-A/1
PD 16-MAR-1999
PF 14-APR-1998 JP 1998103178
PR 08-NOV-1990 US 611.965,09-NOV-1990 US 611.419 PR
13-SEP-1991 US 758.880
PI ROBERT O RARUSUTON,FRANK MARCUS,KENT B SUDIAMU, PI BARBARA A
JABASU,JOHN A HALL
PC C07K14/18,A61K39/29,G01N33/576//C12N15/09,C12P21/02, PC
C12R1.911,
CC C12N15/00
FH Key Location/Qualifiers
FT CDS (342)..(9377).
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Location/Qualifiers
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Query Match 52.4%; Score 834.8; DB 6; Length 9401;
Best Local Similarity 96.4%; Pred. No. 3.3e-220;
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 27 CTGTGTGCTGCTGTGTGGAGAGCTCTTCCTGCGCCAGCGGTAGGAAACCCACGT 86
DB 1442 CTGGCGAAGGCTCTGTGTGTCTGTCTATTTGCGCGCTCGAGCGGAAACCCACGT 1501
QY 87 CACCGGGGAAGTCCCGGCACACTGTGTCTGATTTGTAGCTCTCGACACAGGCG 146
DB 1502 CACCGGGGAAGTCCCGGCACACTGTGTCTGATTTGTAGCTCTCGACACAGGCG 1561
QY 147 CAAGCAGAACGTCACGCTGATCAACACCAACGAGCTTGGCACCTCAATAGCACGCGCT 206
DB 1562 CAAGCAGAACGTCACGCTGATCAACACCAACGAGCTTGGCACCTCAATAGCACGCGCT 1621
QY 207 GAACTCAGATGATAGCTCAACACCGGCTGTTGGCAGGCTTTCCTATCACCACAGTT 266
DB 1622 GAACTCAGATGATAGCTCAACACCGGCTGTTGGCAGGCTTTCCTATCACCACAGTT 1681
QY 267 GAACTCAGATGATAGCTCAACACCGGCTGTTGGCAGGCTTTCCTATCACCACAGTT 326
DB 1682 GAACTCAGATGATAGCTCAACACCGGCTGTTGGCAGGCTTTCCTATCACCACAGTT 1741
QY 327 GGGCTGGGCGCTTATCAGTTATGCCAACGAGCGGCGCCCGACAGCGCCCTTACTGCTG 386
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DB 1802 GCACTACCCCGCCAAAACCTTGGCGGTATTTGTCGGCGAAGAGTGTGTGTCGGGTATA 1861
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2042 TCCTTGTGTCAATCGAGGGGCGGCAACAACACCTCGACTGCGCCCACTGATTGCTTCCG 2101
687 CAACATCCGACCGACCATACTCTCGTGGCGCTCGGTCTCTGGATCAACACCGAGTG 746
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DEFINITION Sequence 9 from patent US 5683864.
ACCESSION I71894
VERSION I71894.1 GI:3008033
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 9401)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Combinations of hepatitis C virus (HCV) antigens for use in
immunoassays for anti-HCV antibodies
JOURNAL Patent: US 5683864-A 9 04-NOV-1997;
FEATURES Location/Qualifiers
Source 1..9401
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ORIGIN
Query Match 52.4%; Score 834.8; DB 6; Length 9401;
Best Local Similarity 96.4%; Pred. No. 3.3e-220;
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 27 CTGTGTGCTGCTGTGTGGAGAGCTCTTCCTGCGCCAGCGGTAGGAAACCCACGT 86
DB 1442 CTGGCGAAGGCTCTGTGTGTCTGTCTATTTGCGCGCTCGAGCGGAAACCCACGT 1501
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DB 1502 CACCGGGGAAGTCCCGGCACACTGTGTCTGATTTGTAGCTCTCGACACAGGCGC 1561
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QY 327 GGGCTGGGCGCTTATCAGTTATGCCAACGAGCGGCGCCCGACAGCGCCCTTACTGCTG 386
DB 1742 GGGCTGGGCGCTTATCAGTTATGCCAACGAGCGGCGCCCGACAGCGCCCTTACTGCTG 1801
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Db	1862	TTGCTTCACTCCAGCCCGTGTGGTGGGAAACGACAGGTTCGGGCGGCCACCTA	1921
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Qy	687	CAAGCATCCGGACGCCACATACTCTCGGTGGGGTCCGGTCCCTGGATCAACCCAGGTG	746
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Db	2222	TAAATCAGGATGTACGTGGAGGGGTGGAACACAGGCTGGAAGCTGCCCTGCAACTGGAC	2281
Qy	867	GCGGGCGAAGCGTTGCGATCTGGAAGATAGGGACAGGTCCGAGATC	912
Db	2282	GCGGGCGAAGCGTTGCGATCTGGAAGATAGGGACAGGTCCGAGATC	2327

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GenCore version 5.1.6  
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Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: Geneseqn1990s:\*
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- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
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- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	834.8	52.4	1207	2	AAQ40330 Sequence
5	834.8	52.4	8316	2	AAQ05955 Hepatitis
6	834.8	52.4	8316	3	AAV5296 cDNA sequ
7	834.8	52.4	8316	12	Adn35977 HCV cDNA
8	834.8	52.4	9185	2	Aaq05956 Sense str
9	834.8	52.4	9185	2	AAQ10566 Hepatitis
10	834.8	52.4	9185	2	AAQ00459 Hepatitis
11	834.8	52.4	9185	2	Aax26737 Nucleotid
12	834.8	52.4	9185	2	Adf66068 Hepatitis
13	834.8	52.4	9185	3	AAV5297 Sense str
14	834.8	52.4	9401	2	Aat12710 Hepatitis
15	834.8	52.4	9401	2	Aat99981 HCV polyp
16	834.8	52.4	9401	2	AAV09989 HCV polyp
17	834.8	52.4	9401	6	AAV35043 Hepatitis
18	834.8	52.4	9401	12	Ad123106 Hepatitis
19	834.8	52.4	9401	13	Adr29358 Hepatitis
20	833.2	52.3	1914	8	AB270946 Hepatitis

21	833.2	52.3	1914	8	ACC71824	Acc71824 HCV-1 E1/
22	833.2	52.3	1914	12	ADO00769	Ado00769 HCV-1 E1/
23	833.2	52.3	9185	12	ADN35979	Adn35979 HCV cDNA
24	833.2	52.3	9379	2	AAQ36209	Aaq36209 Composite
25	833.2	52.3	9400	2	AAQ21744	Aaq21744 Compiled
26	818.8	51.4	9618	11	ADN33102	Adn33102 Hepatitis
27	811.8	51.0	9133	2	AAZ07656	Aaz07656 Nucleotid
28	748.4	47.0	1207	2	AAQ40331	Aaq40331 Sequence
29	745.2	46.8	9646	6	AAV59361	AAV59361 Hepatitis
30	745.2	46.8	9646	6	ABK87285	Abk87285 cDNA enco
31	745.2	46.8	9646	8	ACA62466	Ac62466 HCV H77 C
32	745.2	46.8	11674	3	AAZ36210	Aaz36210 Nucleotid
33	745.2	46.8	12980	2	AAV59364	AAV59364 Hepatitis
34	745.2	46.8	12980	6	ABK87286	Abk87286 Hepatitis
35	745.2	46.8	12980	8	ACA62469	Ac62469 DNA encod
36	745.2	46.8	13198	3	AAZ36211	Aaz36211 Nucleotid
37	745.2	46.8	16622	3	AAZ36212	Aaz36212 Nucleotid
38	742	46.6	1845	12	ADJ10455	Adj10455 DNA of th
39	742	46.6	2517	12	ADJ10457	Adj10457 DNA of th
40	742	46.6	9599	2	AAZ24832	Aaz24832 Infectiou
41	742	46.6	9599	4	AAF23491	Aaf23491 Infectiou
42	742	46.6	9599	4	AAAC6938	Aac6938 Nucleotid
43	742	46.6	9599	12	ADJ56743	Adj56743 Hepatitis
44	742	46.6	9599	12	ADJ64255	Adj64255 Hepatitis
45	742	46.6	10803	10	ADD67945	Add67945 Modified

## ALIGNMENTS

### RESULT 1

AAD06793

ID AAD06793 standard; DNA; 5882 BP.

XX AAD06793;

XX 06-AUG-2001 (first entry)

XX Plasmid pCMV-II-E2661-SAG.

XX Virus-like particle; immunogen; hepatitis B virus surface antigen; HBsAg;  
 KW HBV; chimeric antigen; hepatitis C virus; HCV; virucide; vaccine;  
 KW plasmid pCMV-II-E2661-SAG; cyclic; circular; ds.

XX Human cytomegalovirus.

OS Homo sapiens.

OS Hepatitis C virus.

OS Hepatitis B virus.

OS Bos sp.

OS Unidentified.

OS Chimeric.

XX Key Location/Qualifiers

FT CDS 1992..3587

FT /tag= a

FT /product= "HCV 661 E2 envelope glycoprotein-HBsAg S

FT domain"

FT misc\_feature 1992..2900

FT /tag= b

FT /note= "661 E2 coding sequence from HCV"

FT misc\_feature 2907..3587

FT /tag= c

FT /note= "HBsAg S domain coding sequence from HBV"

XX WO200138358-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US032249.

XX 24-NOV-1999; 99US-0167224P.

XX (CHIR ) CHIRON CORP.

PA





XX 06-MAY-1997; 97US-0045675P.  
 PR (CHIR ) CHIRON CORP.  
 XX  
 PI Houghton M, Choo Q, Abrignani S, Chien D, Selby M, Glazer E;  
 XX  
 XX WPI; 1999-034724/03.  
 DR P-PSDB; AAW67615.  
 XX  
 PT Methods for isolating truncated HCV E1 and E2 polypeptides - used in,  
 PT e.g. immunodiagnostic kits for diagnosis of HCV infection.  
 XX  
 PS Disclosure; Fig 2A-E; 65pp; English.  
 XX  
 CC This sequence represents the coding region for the Hepatitis C virus  
 CC (HCV) E2 protein. The invention relates to the intracellular production  
 CC and isolation of C-terminally truncated variants of the E2 protein. The  
 CC truncations start from about amino acid residue 500 of the E2 protein and  
 CC are generated by PCR amplification of the gene sequence. The truncated  
 CC proteins are then produced intracellularly in host cells which are  
 CC disrupted. The HCV proteins are then purified preferably by affinity  
 CC chromatography, especially using Galanthus nivalis agglutinin resin. The  
 CC HCV E1 and HCV E2 polypeptides can be used to manufacture a medicament  
 CC useful for detecting the presence or absence of HCV infection in an  
 CC individual. They can also be used in a immunodiagnostic test kit for  
 CC detecting HCV infection  
 XX  
 SQ Sequence 1989 BP; 372 A; 586 C; 569 G; 462 T; 0 U; 0 Other;  
 Query Match 52.5%; Score 836.4; DB 2; Length 1989;  
 Best Local Similarity 96.5%; Pred. No. 2.4e-133;  
 Matches 855; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
 XX 27 CTGTGTGCTGCTGTGTGAGCAGTCTTCGTTTCGCCCGCAGCGCTAGCGAAACCCACGT 86  
 Db 12 CTGGCGAAGGTCCTGTAGTGTCTGTCTATTTCGGGGTGCAGCGGAAACCCACGT 71  
 XX 87 CACCGGGGAAGTGC CGGCACACTGTGTCTGTGATTTGTAGCTCTCTCGCACCGGC 146  
 Db 72 CACCGGGGAAGTGC CGGCACACTGTGTCTGTGATTTGTAGCTCTCTCGCACCGGC 131  
 XX 147 CAAGCAGACGTCACGTGATCAACACCAACGACGTCGACCTCAATAGACGCGCCT 206  
 Db 132 CAAGCAGACGTCACGTGATCAACACCAACGACGTCGACCTCAATAGACGCGCCT 191  
 XX 207 GAACTGCAATGATAGCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCACCACAAGTT 266  
 Db 192 GAACTGCAATGATAGCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCACCACAAGTT 251  
 XX 267 CAACTCTTCAGGCTGTCTGAGAGGCTAGCCAGTCCGACCCCTTACCGATTGTGACCA 326  
 Db 252 CAACTCTTCAGGCTGTCTGAGAGGCTAGCCAGTCCGACCCCTTACCGATTGTGACCA 311  
 XX 327 GGGCTGGGCGCTTACGTATGCAACGAGAGCGGCCCGGACCGCCCTACTGCTG 386  
 Db 312 GGGCTGGGCGCTTACGTATGCAACGAGAGCGGCCCGGACCGCCCTACTGCTG 371  
 XX 387 GCACTACCCCGGCAAACTTGGGTATTTGTCGGCGAAGAGTGTGTGTGTCGGTATA 446  
 Db 372 GCACTACCCCGGCAAACTTGGGTATTTGTCGGCGAAGAGTGTGTGTGTCGGTATA 431  
 XX 447 TTGCTTCACTCCAGCCCGTGTGTGGGAACGACCGACAGTCCGGCGCGCCACCTA 506  
 Db 432 TTGCTTCACTCCAGCCCGTGTGTGGGAACGACCGACAGTCCGGCGCGCCACCTA 491  
 XX 507 CAGCTGGGTGAAATGATCGACGCTCTCGTCTTACATACACGACCGCCGCTGG 566  
 Db 492 CAGCTGGGTGAAATGATCGACGCTCTCGTCTTACATACACGACCGCCGCTGG 551  
 XX 567 CAACTGGTTCGGTGTGACCTGGATGAACCTCAACTGGATTCAACAAAGTGTGGGACGCG 626  
 Db 552 CAACTGGTTCGGTGTGACCTGGATGAACCTCAACTGGATTCAACAAAGTGTGGGACGCG 611

QY 627 TCCTTGTGTCTCGAGGGGGGCAACAAACACCTGCACTGCCCCACTGATTGCTTCG 686  
 Db 612 TCCTTGTGTCTCGAGGGGGGCAACAAACACCTGCACTGCCCCACTGATTGCTTCG 671  
 QY 687 CAAGCATCCGAGCGCCACATCTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTG 746  
 Db 672 CAAGCATCCGAGCGCCACATCTCTCGGTGCGGCTCCGGTCCCTGGATCACACCCAGGTG 731  
 QY 747 CTGTGTGACATACCCGTATAGCTTTGGCATTTATCTTGTATCCATCAACTACCATATT 806  
 Db 732 CTGTGTGACATACCCGTATAGCTTTGGCATTTATCTTGTATCCATCAACTACCATATT 791  
 QY 807 TAAATTCAGGATGTACGTGGGAGGGTGCMAACACAGGCTGGAGCTGCTGCAACTGGAC 866  
 Db 792 TAAATTCAGGATGTACGTGGGAGGGTGCMAACACAGGCTGGAGCTGCTGCAACTGGAC 851  
 QY 867 GCGGGGCGAACTTCGATCTGGAAGATAGGACAGGTCCGAGATC 912  
 Db 852 GCGGGGCGAACTTCGATCTGGAAGATAGGACAGGTCCGAGCTC 897  
 RESULT 4  
 AAQ40330  
 ID AAQ40330 standard; cDNA; 1207 BP.  
 XX AC AAQ40330;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 09-AUG-1993 (first entry)  
 XX  
 DE Sequence encoding glycoprotein E2/NS1 in clone HCV1.  
 XX  
 KW Hepatitis C virus; envelope protein; glycoprotein; E2/NS1;  
 KW diagnostic reagent; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 2..1207  
 FT /\*tag= a  
 XX  
 PN EP537626-A1.  
 XX  
 PD 21-APR-1993.  
 XX  
 PF 08-OCT-1992; 92EP-00117191.  
 XX  
 PR 08-OCT-1991; 91JP-00260824.  
 XX  
 PA (NAHE-) NAT INST OF HEALTH.  
 XX  
 PI Miyamura T, Saito I, Harada S, Honda Y;  
 XX  
 DR WPI: 1993-127516/16.  
 DR P-PSDB; AAR34438.  
 XX  
 PT Diagnostic reagent for hepatitis C virus - comprises second envelope  
 PT protein or first non-structural protein encoded by HCV gene and has sugar  
 PT chain.  
 XX  
 PS Claim 8; Page 30-32; 58pp; English.  
 XX  
 CC Glycoprotein E2/NS1 is derived from the second envelope protein or first  
 CC non-structural protein encoded by the genome of HCV. The nucleic acid is  
 CC extracted from the serum of the patient of hepatitis C. The serum is  
 CC pref. mixed with transfer RNA (tRNA) as a carrier of virus RNA. As a  
 CC technique of cloning cDNA from the nucleic acid, it is preferred to use  
 CC polymerase chain reaction method. In the reaction, any commercially  
 CC available random primers or synthesized DNA having a base sequence  
 CC similar to that of primer AS1 may be used as a primer. Representative  
 CC examples of sense primers include S1. (Updated on 25-MAR-2003 to correct  
 CC PN field.)

XX SQ Sequence 1207 BP; 241 A; 369 C; 336 G; 261 T; 0 U; 0 Other;  
 Query Match 52.4%; Score 834.8; DB 2; Length 1207;  
 Best Local Similarity 96.4%; Pred. No. 4.9e-133;  
 Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 QY 27 CTGTGTGCTGCTGCTGTGGAGCAGTCTTTCGTTTCGCCCGAGCGCTAGCGAAACCCACGT 86  
 DB 85 CTGGCGAAGGCTCTGCTAGTGTCTGTCTATTTGCGCGCTGCGACGGGAAACCCACGT 144  
 QY 87 CACCGGGGAAGTGCCTGGCCACACTGTCTGTGGATTGTAGCTCTCGCACCGGCGC 146  
 DB 145 CACCGGGGAAGTGCCTGGCCACACTGTCTGTGGATTGTAGCTCTCGCACCGGCGC 204  
 QY 147 CAAGCAGAAGCTCCAGCTGATCAACACCAACGCGAGTGGCAGCTCAATAGCAGCGCCCT 206  
 DB 205 CAAGCAGAAGCTCCAGCTGATCAACACCAACGCGAGTGGCAGCTCAATAGCAGCGCCCT 264  
 QY 207 GAACCTGCAATGATAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTT 266  
 DB 265 GAACCTGCAATGATAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTT 324  
 QY 267 CAACCTTCAGGCTGTCTGAGAGGCTAGCAGCTGCGGACCCCTTACCGATTGTGACCA 326  
 DB 325 CAACCTTCAGGCTGTCTGAGAGGCTAGCAGCTGCGGACCCCTTACCGATTGTGACCA 384  
 QY 327 GGGCTGGGGCCCTATCAGTTATGCCAAGGAGCGGCCCGGACCGCCCTACTGTGTG 386  
 DB 385 GGGCTGGGGCCCTATCAGTTATGCCAAGGAGCGGCCCGGACCGCCCTACTGTGTG 444  
 QY 387 GCACCTACCCCCCAAACTTGGGTATTTGCGCGGAGAGTGTGTGTCGCGTATA 446  
 DB 445 GCACCTACCCCCCAAACTTGGGTATTTGCGCGGAGAGTGTGTGTCGCGTATA 504  
 QY 447 TTGCTTCACTCCAGGCCCGTGTGTGGGAAGCAGCAGGTGGGGCGGCCACCTA 506  
 DB 505 TTGCTTCACTCCAGGCCCGTGTGTGGGAAGCAGCAGGTGGGGCGGCCACCTA 564  
 QY 507 CAGCTGGGGTGAATATGATACGAGCTCTTCCTTAACTAACATACAGCCACCGCTGG 566  
 DB 565 CAGCTGGGGTGAATATGATACGAGCTCTTCCTTAACTAACATACAGCCACCGCTGG 624  
 QY 567 CAATTGGTTCGTTGCTGATGAACTCAACTGATTTACCAAGTGTGCGAGCGCC 626  
 DB 625 CAATTGGTTCGTTGCTGATGAACTCAACTGATTTACCAAGTGTGCGAGCGCC 684  
 QY 627 TCCTTGTGTCATCGAGGGCGGGCAACACCTGTGACTGCCCGCAGTGTCTCG 686  
 DB 685 TCCTTGTGTCATCGAGGGCGGGCAACACCTGTGACTGCCCGCAGTGTCTCG 744  
 QY 687 CAAGCATCCGAGCGGCACATCTCGGTGGGCTCCGTCCTCGATCACACCCAGGTG 746  
 DB 745 CAAGCATCCGAGCGGCACATCTCGGTGGGCTCCGTCCTCGATCACACCCAGGTG 804  
 QY 747 CCGTGTGCACTACCGGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACCATATT 806  
 DB 805 CCGTGTGCACTACCGGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACCATATT 864  
 QY 807 TAAATATCAGGATGATAGTGGAGGGTGGAAACAGGCTGGAGCTGCTGCAACTGGAC 866  
 DB 865 TAAATATCAGGATGATAGTGGAGGGTGGAAACAGGCTGGAGCTGCTGCAACTGGAC 924  
 QY 867 GCGGGGCGAAGCTTCGGATCTGGAAGATAGGACAGGTCCGAGATC 912  
 DB 925 GCGGGGCGAAGCTTCGGATCTGGAAGATAGGACAGGTCCGAGATC 970  
 RESULT 5  
 AAQ05955  
 ID AAQ05955 standard; cDNA; 8316 BP.  
 XX  
 AC AAQ05955;

XX 25-MAR-2003 (revised)  
 DT 23-JAN-1991 (first entry)  
 XX Hepatitis C virus open reading frame.  
 DE Hepatitis C virus; antiviral agent; ds.  
 KW Hepatitis C virus.  
 OS Hepatitis C virus.  
 XX EP388232-A.  
 XX 19-SEP-1990.  
 XX 16-MAR-1990; 90EP-00302866.  
 XX 17-MAR-1989; 89US-00325338.  
 PR 20-APR-1989; 89US-00341334.  
 PR 18-MAY-1989; 89US-00355002.  
 XX (CHIR ) CHIRON CORP.  
 PA Houghton M, Choo QL, Kuo G;  
 PI WPI; 1990-284418/38.  
 DR P-PSDB; AAR08123.  
 XX Hepatitis C virus DNA - used for producing probes, polypeptide(s),  
 PT antibodies and anti-sense polynucleotide(s) for diagnosis and therapy.  
 PS Disclosure; Fig 16; 83pp; English.  
 XX HCV cDNA libraries were constructed using pooled serum from a chimpanzee  
 CC with chronic HCV infection. A lambda gtl library was screened with  
 CC probes derived from previously isolated clones. The ORF is derived from  
 CC the overlapping clones p14a, CA167b, CA156e, CA84a, CA59a, K9-1, 12f,  
 CC 14i, 11b, 7f, 8h, 33c, 40b, 37b, 36, 81, 32, 33b, 25c, 14c, 8f, 33f,  
 CC 33g, 35c, 35f, 19g, 26g and 15e. Polypeptide encoded by this sequence can  
 CC be used to design probes for the detection of HCV nucleic acids, in  
 CC screening programmes for antiviral agents and in preparing blood free of  
 CC HCV. Antisense polynucleotides can be used to inhibit viral replication.  
 CC See also AAQ05956. (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 8316 BP; 1671 A; 2529 C; 2345 G; 1771 T; 0 U; 0 Other;  
 Query Match 52.4%; Score 834.8; DB 2; Length 8316;  
 Best Local Similarity 96.4%; Pred. No. 3.6e-133;  
 Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 QY 27 CTGTGTGCTGCTGCTGTGGAGCAGTCTTTCGTTTCGCCCGAGCGCTAGCGAAACCCACGT 86  
 DB 759 CTGGCGAAGGCTCTGTTAGTGTCTGCTCTATTTGCCGGCTGAGCGGAAACCCACGT 818  
 QY 87 CACCGGGGAAGTGCCTGGCCACACTGTCTGTGGATTGTAGCTCTCTCGCACCGGCGC 146  
 DB 819 CACCGGGGAAGTGCCTGGCCACACTGTCTGTGGATTGTAGCTCTCTCGCACCGGCGC 878  
 QY 147 CAAGCAGAAGCTCCAGCTGATCAACACCAACGCGAGTGGCAGCTCAATAGCAGCGCCCT 206  
 DB 879 CAAGCAGAAGCTCCAGCTGATCAACACCAACGCGAGTGGCAGCTCAATAGCAGCGCCCT 938  
 QY 207 GAACCTGCAATGATAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTT 266  
 DB 939 GAACCTGCAATGATAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTT 998  
 QY 267 CAACCTTCAGGCTGTCTGAGAGGCTAGCAGCTGCGGACCCCTTACCGATTGTGACCA 326  
 DB 999 CAACCTTCAGGCTGTCTGAGAGGCTAGCAGCTGCGGACCCCTTACCGATTGTGACCA 1058  
 QY 327 GGGCTGGGGCCCTATCAGTTATGCCAAGGAGGGGCCCGGACCGCCCTACTGTGTG 386  
 DB 1059 GGGCTGGGGCCCTATCAGTTATGCCAAGGAGGGGCCCGGACCGCCCTACTGTGTG 1118

QY 387 GCACCTACCCCAAAACCTTCGGGTATTGTGCCCGGAAGAGTGTGTGTCGGGTATA 446  
 DB 1119 GCACCTACCCCAAAACCTTCGGGTATTGTGCCCGGAAGAGTGTGTGTCGGGTATA 1178  
 QY 447 TTGCTTCACTCCAGCCCCGTCGGTGTGGGAACGACGACAGGTGCGGCGCCACCTA 506  
 DB 1179 TTGCTTCACTCCAGCCCCGTCGGTGTGGGAACGACGACAGGTGCGGCGCCACCTA 1238  
 QY 507 CAGCTGGGTGAATATGATAGGAGCTCTTCGTCCTTAACAAATACAGGCCACCGCTGGG 566  
 DB 1239 CAGCTGGGTGAATATGATAGGAGCTCTTCGTCCTTAACAAATACAGGCCACCGCTGGG 1298  
 QY 567 CAATTGGTTCGGTGTACTCGATGAATCAACTGATTTACCAAGTGTGCGGAGCGCC 626  
 DB 1299 CAATTGGTTCGGTGTACTCGATGAATCAACTGATTTACCAAGTGTGCGGAGCGCC 1358  
 QY 627 TCCTTGTGTCACTCGAGGGGGGCAACACACCTGCACTGCCCACTGATTGCTTCG 686  
 DB 1359 TCCTTGTGTCACTCGAGGGGGGCAACACACCTGCACTGCCCACTGATTGCTTCG 1418  
 QY 687 CAAGCATCGGACGCCACATCTCTCGTGGGCTCCGTCCTGGATCAACCCAGGTG 746  
 DB 1419 CAAGCATCGGACGCCACATCTCTCGTGGGCTCCGTCCTGGATCAACCCAGGTG 1478  
 QY 747 CCTGTCGACTACCCGTATAGGCTTTGGCATTTATCTTTGTACCATCAACTACCATATT 806  
 DB 1479 CCTGTCGACTACCCGTATAGGCTTTGGCATTTATCTTTGTACCATCAACTACCATATT 1538  
 QY 807 TAAATATCAGGATGTACGTGGGAGGGTCGAACACAGGCTGGAAGCTGCACTGCACTGAC 866  
 DB 1539 TAAATATCAGGATGTACGTGGGAGGGTCGAACACAGGCTGGAAGCTGCACTGCACTGAC 1598  
 QY 867 GCGGGCGCAACGTTGCGATCTGGAAGATAGGACAGGTCCGAGATC 912  
 DB 1599 GCGGGCGCAACGTTGCGATCTGGAAGATAGGACAGGTCCGAGATC 1644

RESULT 6

AAA75296  
 ID AAA75296 standard; cDNA; 8316 BP.

XX AAA75296;

XX 15-JAN-2001 (first entry)

XX cDNA sequence compiled Hepatitis C virus cDNA clones.

XX Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;  
 XX viral infectivity; viral replication; ds.

XX Hepatitis C virus.

XX Key Location/Qualifiers  
 FH 1..8316  
 FT /\*tag= a  
 FT /note= "partial sequence; no termination codon given"

XX EP1034785-A2.

XX 13-SEP-2000.

XX 16-MAR-1990; 2000EP-00109602.

XX 17-MAR-1989; 89US-00325338.

PR 20-APR-1989; 89US-00341334.

PR 18-MAY-1989; 89US-00355002.

PR 16-MAR-1990; 90EP-00302866.

XX (CHIR ) CHIRON CORP.

XX Houghton M, Choo Q, Kuo G;

XX WPI; 2000-566891/53.

DR P-PSDB; AAB18540.  
 XX Novel composition comprising a hepatitis C virus antisense polynucleotide  
 PT which is complementary to or corresponds to a sense strand of the virus  
 PT genome, and selectively hybridizes to it.  
 PS Example; Fig 16; 75pp; English.  
 XX The specification describes a pharmaceutical composition which comprises  
 CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is  
 CC characterized by a positive stranded RNA genome which has 40% homology at  
 CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide  
 CC binds to cellular polynucleotides which enhance and/or are required for  
 CC viral infectivity, replicative ability or chronicity. The antisense  
 CC polynucleotides may also be designed to bind with high specificity, to be  
 CC of increased stability, to be stable and to have low toxicity. The  
 CC composition also comprises an agent which causes viral RNA to be  
 CC inactive. The composition is used for preventing HCV replication in a  
 CC system. The present sequence represents a novel HCV cDNA sequence, which  
 CC is used in the course of the invention  
 XX Sequence 8316 BP; 1671 A; 2529 C; 2345 G; 1771 T; 0 U; 0 Other;

Query Match 52.4%; Score 834.8; DB 3; Length 8316;  
 Best Local Similarity 96.4%; Pred. No. 3.6e-133;  
 Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 27 CTGTGTGCTGCTGTGTGGAGCAGTCTTCGTTTGCCTCCAGCGCTAGCAAAACCCAGT 86  
 DB 759 CTGGCGGAGTCTGTGTAGTGTCTATTTCGCGGCTGCGACGGGAAACCCAGT 818  
 QY 87 CACCGGGGAAGTGC CGGCCACACTGTGTCTGGAATTTGTAGCTCTTCGACACGAGGC 146  
 DB 819 CACCGGGGAAGTGC CGGCCACACTGTGTCTGGAATTTGTAGCTCTTCGACACGAGGC 878  
 QY 147 CAACGAGAACGTCAGCTGATCAACCAACGAGTTGGCACCTCAATAGCACCGCCCT 206  
 DB 879 CAACGAGAACGTCAGCTGATCAACCAACGAGTTGGCACCTCAATAGCACCGCCCT 938  
 QY 207 GAACCTGCAATGATAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCAAGTT 266  
 DB 939 GAACCTGCAATGATAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCAAGTT 998  
 QY 267 CAACCTTTCAAGCTGTCTGTAGAGCTAGCAGCTGCCGACCCCTTACGATTTTGACCA 326  
 DB 999 CAACCTTTCAAGCTGTCTGTAGAGCTAGCAGCTGCCGACCCCTTACGATTTTGACCA 1058  
 QY 327 GGGCTGGGGCCCTATCAGTTATGCCAAGGGGGCCCGACAGCGCCCTACTGCTG 386  
 DB 1059 GGGCTGGGGCCCTATCAGTTATGCCAAGGGGGCCCGACAGCGCCCTACTGCTG 1118  
 QY 387 GCACCTACCCCAAAACCTTCGGGTATTGTGCCCGGAAGAGTGTGTGTGTCGGGTATA 446  
 DB 1119 GCACCTACCCCAAAACCTTCGGGTATTGTGCCCGGAAGAGTGTGTGTGTCGGGTATA 1178  
 QY 447 TTGCTTCACTCCAGCCCCGTCGGTGTGGGAACGACGACAGGTGCGGCGCCACCTA 506  
 DB 1179 TTGCTTCACTCCAGCCCCGTCGGTGTGGGAACGACGACAGGTGCGGCGCCACCTA 1238  
 QY 507 CAGCTGGGTGAATATGATAGGAGCTCTTCGTCCTTAACAAATACAGGCCACCGCTGGG 566  
 DB 1239 CAGCTGGGTGAATATGATAGGAGCTCTTCGTCCTTAACAAATACAGGCCACCGCTGGG 1298  
 QY 567 CAATTGGTTCGGTGTACTCGATGAATCAACTGATTTACCAAGTGTGCGGAGCGCC 626  
 DB 1299 CAATTGGTTCGGTGTACTCGATGAATCAACTGATTTACCAAGTGTGCGGAGCGCC 1358  
 QY 627 TCCTTGTGTCACTCGAGGGGGGCAACACACCTGCACTGCCCACTGATTGCTTCG 686  
 DB 1359 TCCTTGTGTCACTCGAGGGGGGCAACACACCTGCACTGCCCACTGATTGCTTCG 1418  
 QY 687 CAAGCATCGGACGCCACATCTCTCGTGGGCTCCGTCCTGGATCAACCCAGGTG 746



Db 1419 CAAGCAATCCGACGCCACATATCTCTCGGTGCGCTCCGGTCCCTGGATCACACCCAGGTG 1478  
QY 747 CTGTGTCGACTACCCGATAGGCTTTGGGATTTATCTTTGATACCATCAACTACACCATATT 806  
Db 1479 CTGTGTCGACTACCCGATAGGCTTTGGGATTTATCTTTGATACCATCAACTACACCATATT 1538  
QY 807 TAAATCAGGATGATCGTGGAGGGTTCGAACACAGGCTGGAACTGCTGCAACTGGAC 866  
Db 1539 TAAATCAGGATGATCGTGGAGGGTTCGAACACAGGCTGGAACTGCTGCAACTGGAC 1598  
QY 867 GCGGGCGAAGCTTGCAGTCTGGAAGTAGGGACAGGTCCGAGATC 912  
Db 1599 GCGGGCGAAGCTTGCAGTCTGGAAGTAGGGACAGGTCCGAGCTC 1644

RESULT 7  
ADN35977  
ID ADN35977 standard; cDNA; 8316 BP.  
XX  
AC ADN35977;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE HCV cDNA clone #1.  
XX  
KW Antiviral; Vaccine; hepatitis C virus infection; HCV infection; ss.  
XX  
OS Hepatitis C virus.  
XX  
PN EP1394255-A2.  
XX  
PD 03-MAR-2004.  
XX  
PF 16-MAR-1990; 2003EP-00016585.  
XX  
PR 17-MAR-1989; 89US-00325338.  
PR 20-APR-1989; 89US-00341334.  
PR 18-MAY-1989; 89US-00355002.  
PR 16-MAR-1990; 90EP-00302866.  
XX  
PA (CHIR ) CHIRON CORP.  
XX  
PI Houghton M, Choo Q, Kuo G;  
XX  
DR WPI; 2004-193149/19.  
DR P-PSDB; ADN35976.  
XX  
PT Novel purified hepatitis C virus polypeptide comprising epitope encoded  
PT by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C  
PT virus.  
XX  
PS Example 1; Fig 16; 79pp; English.  
XX  
XX The present invention relates to hepatitis C virus (HCV) proteins and  
CC cDNA sequences. The sequences are useful in immunoassays for detecting  
CC antibodies directed against HCV antigen; preparing host cells transformed  
CC with a recombinant polynucleotide; screening antiviral agents and  
CC determining the effect of antiviral agent in inhibiting viral replication  
CC in cell culture system; and developing vaccine for treating HCV  
CC infection.  
XX  
SQ Sequence 8316 BP; 1671 A; 2537 C; 2338 G; 1770 T; 0 U; 0 Other;

Query Match 52.4%; Score 834.8; DB 12; Length 8316;  
Best Local Similarity 96.4%; Pred. No. 3.6e-133; Indels 0; Gaps 0;  
Matches 854; Conservative 0; Mismatches 32;  
QY 27 CTGTGTCGCTGCTGTGGAGCAGTCTTCGTTTCGCCGACGCTAGCGAAACCCACGT 86  
Db 759 CTGGGCGAAGTCTCTGGTAGTCTGCTGCTATTTCGCGGCTGACGCGGAACCCACGT 818  
QY 87 CACCGGGGAAGTGGCGGCCACACTGTGTCTGGATTGTTCCTCGCACCGAGGCG 146

Db 819 CACCGGGGAAGTGGCGGCCACACTGTGTCTGGATTGTGTAGCTCTCTGCACACGCGC 878  
QY 147 CAAGCAGAAGCTCCAGCTGATCAACACCAACGCGAGTTCGCACCTCAATAGCACGCGCT 206  
Db 879 CAAGCAGAAGCTCCAGCTGATCAACACCAACGCGAGTTCGCACCTCAATAGCACGCGCT 938  
QY 207 GAATGCAATGATAGCTTCAACACCGGCTGGTTGGCAGGCTTTTCTATCACCACAAGTT 265  
Db 939 GAATGCAATGATAGCTTCAACACCGGCTGGTTGGCAGGCTTTTCTATCACCACAAGTT 998  
QY 267 CAACTCTTCAGGCTGCTGAGAGGTAGCAGCTCCGACCCCTTACCGATTTGACCA 326  
Db 999 CAACTCTTCAGGCTGCTGAGAGGTAGCAGCTCCGACCCCTTACCGATTTGACCA 1058  
QY 327 GGGCTGGGCGCTTATCAGTTATGCCAAACGGAAGCGGCCCCGACGCGCCCTACTGCTG 386  
Db 1059 GGGCTGGGCGCTTATCAGTTATGCCAAACGGAAGCGGCCCCGACGCGCCCTACTGCTG 1118  
QY 387 GCATACCCCCCAAAACCTTTCGGTATTGTGCCGCGAAGAGTGTGTGGTCCGGTATA 446  
Db 1119 GCATACCCCCCAAAACCTTTCGGTATTGTGCCGCGAAGAGTGTGTGGTCCGGTATA 1178  
QY 447 TTGCTTCACTCCAGCCCCGCTGGTGGGAAGCAGCAGGTCCGGGCGCGCCACCTA 506  
Db 1179 TTGCTTCACTCCAGCCCCGCTGGTGGGAAGCAGCAGGTCCGGGCGCGCCACCTA 1238  
QY 507 CAGCTGGGGTGAAATGATACGAGCTCTTCGCTTAAACAATACCAGGCCACCGCTGGG 566  
Db 1239 CAGCTGGGGTGAAATGATACGAGCTCTTCGCTTAAACAATACCAGGCCACCGCTGGG 1298  
QY 567 CAAATTGGTTTCGGTTGTACCTGGATGAATCAACTGGAATTCACCAAGTGTGCGGAGCGCC 626  
Db 1299 CAAATTGGTTTCGGTTGTACCTGGATGAATCAACTGGAATTCACCAAGTGTGCGGAGCGCC 1358  
QY 627 TCCTTGTGTCATCGAGGGGCGGGGCAACAAACCTTGCACTGCCCCCACTGATTGCTTCCG 686  
Db 1359 TCCTTGTGTCATCGAGGGGCGGGCAACAAACCTTGCACTGCCCCCACTGATTGCTTCCG 1418  
QY 687 CAAAGCATCCGAGCGCCACATCTCTCGGTGCGGCTCCGCTCGATCACACCCAGGTG 746  
Db 1419 CAAAGCATCCGAGCGCCACATCTCTCGGTGCGGCTCCGCTCGATCACACCCAGGTG 1478  
QY 747 CCGTGTGCACTACCCGCTATAGCTTTTGGCATTTATCTTGTACCATCAACTACACCATATT 806  
Db 1479 CCGTGTGCACTACCCGCTATAGCTTTTGGCATTTATCTTGTACCATCAACTACACCATATT 1538  
QY 807 TAAATCAGGATGATAGTGGAGGGTTCGAACACAGGCTGGAACTGCTGCAACTGGAC 866  
Db 1539 TAAATCAGGATGATAGTGGAGGGTTCGAACACAGGCTGGAACTGCTGCAACTGGAC 1598  
QY 867 GCGGGCGAAGCTTGCAGTCTGGAAGTAGGGACAGGTCCGAGATC 912  
Db 1599 GCGGGCGAAGCTTGCAGTCTGGAAGTAGGGACAGGTCCGAGCTC 1644

RESULT 8  
AAQ05956  
ID AAQ05956 standard; DNA; 9185 BP.  
XX  
AC AAQ05956;  
XX

DT 25-MAR-2003 (revised)  
DT 23-JAN-1991 (first entry)  
XX  
DE Sense strand of the compiled Hepatitis C virus cDNA sequence.  
XX  
KW Hepatitis C virus (HCV); antiviral agent; ss.  
OS Hepatitis C virus.  
XX  
FH Key Location/Qualifiers  
FT misc\_RNA 1..1667  
FT /\*tag= b

FT CDS /note= "epitope within this region is claimed"  
 FT 320..9185  
 FT /\*tag= a  
 FT misc\_RNA 8978..9185  
 FT /\*tag= c  
 FT /note= "encodes an epitope that is claimed"  
 XX  
 PN EP388232-A.  
 XX  
 XX 19-SEP-1990.  
 PD  
 XX 16-MAR-1990; 90EP-00302856.  
 PF  
 XX 17-MAR-1989; 89US-00325338.  
 PR  
 XX 20-APR-1989; 89US-00341334.  
 PR  
 XX 18-MAY-1989; 89US-00355002.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 XX Houghton M, Choo QL, Kuo G;  
 PI  
 XX WPI; 1990-284418/38.  
 DR  
 DR P-PSDB; AAR08124.  
 XX  
 XX Hepatitis C virus DNA - used for producing probes, polypeptide(s),  
 PT antibodies and anti-sense polynucleotide(s) for diagnosis and therapy.  
 PT  
 XX Disclosure; Fig 17; 83pp; English.  
 PS  
 XX HCV cDNA libraries were constructed using pooled serum from a chimpanzee  
 CC with chronic HCV infection. A lambda gt10 library was screened with  
 CC probes derived from previously isolated clones. The ORF is derived from  
 CC the overlapping clones b114a, ag30a, CA205a, CA290a, CA216a, p14a,  
 CC CA167b, CA156e, CA84a, CA59a, K9-1, 26j, 131, 12f, 141, 11b, 7f, 8h, 33c,  
 CC 40b, 37b, 35, 36, 81, 32, 33b, 25c, 14c, 8f, 33f, 33g, 39c, 35f, 19g, 26g  
 CC 15e, b5a and 16jh. These clones extend the sequence of the HCV genome  
 CC reported in EP-318216. The upstream region from nucleotides -319 to +1348  
 CC (=1-1667 in this file) is covered by clones b114a, 18g, ag30a, CA205a  
 CC CA290a, CA216a, p14a, CA167b, CA156e, CA84a and CA59a; nucleotides 8659-  
 CC 8866 (=8978-9185 in this file) are covered by clones b5a and 16jh. See  
 CC also AAQ05955. (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T; 0 U; 0 Other;  
 Query Match 52.4%; Score 834.8; DB 2; Length 9185;  
 Best Local Similarity 96.4%; Pred. No. 3.6e-133;  
 Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
 QY 27 CTGTGCTGCTGCTGTGGAGCAGTCTTCTGCTTTCGCCCGCGCTAGCGAAACCCACGT 86  
 DB 1420 CTGGGCGAAGGTCCTGTGTAGTCTGCTGTATTTTGGCGCGTGCAGCGGGAACCCACGT 1479  
 QY 87 CACCGGGGAAGTGGCGGCCACACATGTGTCTGGATTTTGTAGCTCTCTCGCACCGAGGC 146  
 DB 1480 CACCGGGGAAGTGGCGGCCACACATGTGTCTGGATTTTGTAGCTCTCTCGCACCGAGGC 1539  
 QY 147 CAAGCAGAACGTCAGCTGATCAACCAACGGCAGTGGCACCCTCAATAGCAGGCCCT 206  
 DB 1540 CAAGCAGAACGTCAGCTGATCAACCAACGGCAGTGGCACCCTCAATAGCAGGCCCT 1599  
 QY 207 GAACGTCAATGATAGCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAAGTT 266  
 DB 1600 GAACGTCAATGATAGCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAAGTT 1659  
 QY 267 CAACTCTTCAGGCTGCTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCAGATTTTGACCA 326  
 DB 1660 CAACTCTTCAGGCTGCTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCAGATTTTGACCA 1719  
 QY 327 GGGCTGGGCGCTTATCAGTTATGCCAACGAGCGGCCCGGACCGCCCTTACTGCTG 386  
 DB 1720 GGGCTGGGCGCTTATCAGTTATGCCAACGAGCGGCCCGGACCGCCCTTACTGCTG 1779  
 QY 387 GCACCTACCCCCCAAAACCTTTCGGGTATTTGTCGCCGGAAGAGTGTGTGTGTCGGGTATA 446

DB 1780 GCACCTACCCCCCAAAACCTTTCGGGTATTTGTCGCCGGAAGAGTGTGTGTGTCGGGTATA 1839  
 QY 447 TTGCTTCACTCCAGCCCCCGTGGTGGGAACACGACGACAGGTGCGGCGCGCCACCTA 506  
 DB 1840 TTGCTTCACTCCAGCCCCCGTGGTGGGAACACGACGAGGTGCGGCGCGCCACCTA 1899  
 QY 507 CAGCTGGGTTGAAATGATACGACGCTCTTCGTCTTTAAACAATACCGAGCCACCGCTGG 566  
 DB 1900 CAGCTGGGTTGAAATGATACGACGCTCTTCGTCTTTAAACAATACCGAGCCACCGCTGG 1959  
 QY 567 CAATTGGTTTCGGTTGTATCTCTGATGAACCTCAACTGGAATTCACCAAGTGTGCGGAGCGCC 626  
 DB 1960 CAATTGGTTTCGGTTGTATCTCTGATGAACCTCAACTGGAATTCACCAAGTGTGCGGAGCGCC 2019  
 QY 627 TCCTTGTGTCACTCGAGGGCGGCAACAACACCTGCACTGCCCACTGATTGCTTCGG 686  
 DB 2020 TCCTTGTGTCACTCGAGGGCGGCAACAACACCTGCACTGCCCACTGATTGCTTCGG 2079  
 QY 687 CAAGCATCCGACGCCACATACCTCTCGGTGGGGTCCGGTCCCTGGATCACACCCAGGTG 746  
 DB 2080 CAAGCATCCGACGCCACATACCTCTCGGTGGGGTCCGGTCCCTGGATCACACCCAGGTG 2139  
 QY 747 CCTGGTCACTACCCGTATAGGCTTTGGCATATTCCTTGTACCATCAACTACCATATT 806  
 DB 2140 CCTGGTCACTACCCGTATAGGCTTTGGCATATTCCTTGTACCATCAACTACCATATT 2199  
 QY 807 TAAATCAGGATGTACGTGGGAGGGTGCACACAGGCTGGAAGCTGCTGCAACTGGAC 866  
 DB 2200 TAAATCAGGATGTACGTGGGAGGGTGCACACAGGCTGGAAGCTGCTGCAACTGGAC 2259  
 QY 867 GCGGGCGAAACGTTGCGATCTGGAAGATAGGACAGGTCGAGATC 912  
 DB 2260 GCGGGCGAAACGTTGCGATCTGGAAGATAGGACAGGTCGAGATC 2305  
 RESULT 9  
 AAQ10566  
 ID AAQ10566 standard; DNA; 9185 BP.  
 XX  
 AC AAQ10566;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 29-APR-1991 (first entry)  
 XX  
 XX Hepatitis C virus strain 1 DNA.  
 DE  
 XX Hepatitis C virus; HCV-1; non-A, non-B hepatitis; HCV antigen;  
 KW viral infections; ss.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN EP414475-A.  
 XX  
 PD 27-FEB-1991.  
 XX  
 XX 21-AUG-1990; 90EP-00309120.  
 PF  
 XX 25-AUG-1989; 89US-00398667.  
 PR  
 XX (CHIR ) CHIRON CORP.  
 PA  
 XX Weiner AJ, Steimer KS;  
 PI  
 XX WPI; 1991-059670/09.  
 DR  
 XX Cell lines infected with hepatitis C virus - are used as source of  
 PT antigens for detection of HCV antibodies, for vaccines, and for screening  
 PT anti-viral agents.  
 XX  
 XX Disclosure; Fig 1; 24pp; English.  
 PS  
 XX This is a hepatitis C virus (HCV) composite cDNA sequence, deduced using

CC overlapping clones. a compsn. contg. the antigenic protein encoded by  
CC this sequence is useful for detecting anti-HCV anti- bodies (Abs) and for  
CC screening an agent which inhibits HCV replic- ation. A cell line infected  
CC with this virus can be used as a source of antigens. The antigen is  
CC useful for preparing vaccines for treating viral infections. See also  
CC AAQ10567. (updated on 25-MAR-2003 to correct PA field.)  
XX

SQ Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T; 0 U; 0 Other;

Query Match 52.4%; Score 834.8; DB 2; Length 9185;  
Best Local Similarity 96.4%; Pred. No. 3.6e-133;  
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 27 CTGTGTGCTGCTGCTGTGTGAGCAGTCTTCGTTTCGCCCGAGCGGTAGCGAAACCCACGT 86  
DB 1420 CTGGCGAAGGCTCTGGTAGTCTGCTGCTATTTCGCGGCGTACGCGGAACCCACGT 1479  
QY 87 CACCGGGGAGTGGCGGCACACCTGTGTCTGATTTGTAGCTCTCTGCAACGAGGC 146  
DB 1480 CACCGGGGAGTGGCGGCACACCTGTGTCTGATTTGTAGCTCTCTGCAACGAGGC 1539  
QY 147 CAAGCAGAACGTCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCACGCGCT 206  
DB 1540 CAAGCAGAACGTCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCACGCGCT 1599  
QY 207 GAATCTGCAATGATAGCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCAAGTT 266  
DB 1600 GAATCTGCAATGATAGCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCAAGTT 1659  
QY 267 CAACTCTTCAGCTGCTGTAGAGGCTAGCAGCTGCGACCCCTTACGATTTGACCA 326  
DB 1660 CAACTCTTCAGCTGCTGTAGAGGCTAGCAGCTGCGACCCCTTACGATTTGACCA 1719  
QY 327 GGGCTGGGCGCTATCAGTTATGCCAAGGAGCGGCCCGACAGCGCCCTACTGCTG 386  
DB 1720 GGGCTGGGCGCTATCAGTTATGCCAAGGAGCGGCCCGACAGCGCCCTACTGCTG 1779  
QY 387 GCATCTACCCCAACCACTTCGGGTATTTGTGCGCGAAGAGTGTGTGTCGGGTATA 446  
DB 1780 GCATCTACCCCAACCACTTCGGGTATTTGTGCGCGAAGAGTGTGTGTCGGGTATA 1839  
QY 447 TTGCTTACTCCAGCGCGCTGTGTGTGGGAACGACAGAGTGGCGGCGGCCACCTA 506  
DB 1840 TTGCTTACTCCAGCGCGCTGTGTGTGGGAACGACAGAGTGGCGGCGGCCACCTA 1899  
QY 507 CAGCTGGGCTGAAATGATACGAGCTCTTCGTCTTAAACATACAGCGCACCGCTGG 566  
DB 1900 CAGCTGGGCTGAAATGATACGAGCTCTTCGTCTTAAACATACAGCGCACCGCTGG 1959  
QY 567 CAATTGGTTTGGTTTACTCTGATGAACCTCAACTGGATTTCACCAAGTGTGGAGCGCC 626  
DB 1960 CAATTGGTTTGGTTTACTCTGATGAACCTCAACTGGATTTCACCAAGTGTGGAGCGCC 2019  
QY 627 TCCTTGTGTATCGAGGGCGGCAACACCTGTGATGCTGCCCACTGATTTGTCG 686  
DB 2020 TCCTTGTGTATCGAGGGCGGCAACACCTGTGATGCTGCCCACTGATTTGTCG 2079  
QY 687 CAAGCATCCGAGCGCACATCTCTCGGTGGGCTCCGCTCCGATCAGACCCAGGTG 746  
DB 2080 CAAGCATCCGAGCGCACATCTCTCGGTGGGCTCCGCTCCGATCAGACCCAGGTG 2139  
QY 747 CTGTGTGACTACCGGTATAGCTTTTGGCATTTATCTTTGTACCATCAACTACCATATT 806  
DB 2140 CTGTGTGACTACCGGTATAGCTTTTGGCATTTATCTTTGTACCATCAACTACCATATT 2199  
QY 807 TAAATCAGGATGTAGTGGAGGGGTGAAACAGAGGTGGAAGCTGCTGCACTGAC 866  
DB 2200 TAAATCAGGATGTAGTGGAGGGGTGAAACAGAGGTGGAAGCTGCTGCACTGAC 2259  
QY 867 GCGGGGCAACGTTGCGATCTGGAGATAGGAGACAGGTCCGAGATC 912  
DB 2260 GCGGGGCAACGTTGCGATCTGGAGATAGGAGACAGGTCCGAGATC 2305

RESULT 10

AXX00459  
ID AAX00459 standard; DNA; 9185 BP.

XX AC AAX00459;  
XX

DT 10-MAY-1999 (first entry)

XX Hepatitis C virus 1 ORF1.

XX HCV; non-A, non-B hepatitis; NANBH; diagnosis; vaccine; antigen;  
KW antibody; immunoassay; assay; ss.

XX Hepatitis C virus.

XX Key Location/Qualifiers  
FT CDS 320..9185  
/\*tag= a

XX US5856437-A.

XX 05-JAN-1999.

XX 03-NOV-1994; 94US-00334255.

XX 15-SEP-1989; 89US-00408045.

XX 21-DEC-1989; 89US-00456142.

XX 04-JAN-1991; 91US-00637380.

XX 02-AUG-1993; 93US-00101280.

XX 24-FEB-1994; 94US-00201066.

XX (NAHE-) NAT INST OF HEALTH JAPAN.  
XX (CHIR-) CHIRON CORP.

XX Weiner AJ, Miyamura T, Irvine BD, Kolberg JA, Han J, Saito I;  
PI Cha T, Houghton M;  
XX WPI; 1999-105191/09.

XX Antigenic polypeptides from J1 and J7 hepatitis C virus isolates - useful  
PT as immunoassay reagents, for raising antibodies and as vaccine  
PT components.

XX Disclosure; Fig 12A-C; 44pp; English.

XX This is the nucleotide sequence of ORF1 of hepatitis C virus prototype  
CC HCV-1. The invention relates to 2 new isolates, J1 and J7, of HCV. These  
CC new isolates comprise nucleotide (see AAX00400-04) and amino acid (see  
CC AAW30583-87) sequences which are distinct from HCV1. Thus J1 and J7  
CC provide new polynucleotides and polypeptides useful in diagnostics,  
CC recombinant protein production and vaccine development. Claimed  
CC polypeptides can be used: (i) as immunoassay reagents, or standards, to  
CC detect HCV antibodies, e.g. for diagnosing infection or screening donated  
CC blood; (ii) to generate specific antibodies (used for detecting the  
CC corresponding polypeptide, to screen for antiviral agents, for virus  
CC isolation and for passive immunisation); (iii) in protective or  
CC therapeutic vaccines, and (iv) for isolation of non-A, non-B viruses  
XX

SQ Sequence 9185 BP; 1849 A; 2793 C; 2605 G; 1938 T; 0 U; 0 Other;  
Query Match 52.4%; Score 834.8; DB 2; Length 9185;  
Best Local Similarity 96.4%; Pred. No. 3.6e-133;  
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 27 CTGTGTGCTGCTGTGTGTGAGCAGTCTTCGTTTCGCCCGAGCGGTAGCGAAACCCACGT 86  
DB 1420 CTGGCGAAGGCTCTGGTAGTGTCTCTATTTCGCGGCGTCCGACGCGAAACCCACGT 1479

QY 87 CACCGGGGAGTGGCGGCACACCTGTGTCTGGATTTGTTAGCTCTCTCGCACCGAGCGC 146  
DB 1480 CACCGGGGAGTGGCGGCACACCTGTGTCTGGATTTGTTAGCTCTCTCGCACCGAGCGC 1539

QY	147	CAAGCAGAACGTCCTCAGCTGATCAACACCAACGCGCAGTTGGCACCTCAATAGCAGCGCCCT	206
Db	1540	CAAGCAGAACGTCCTCAGCTGATCAACACCAACGCGCAGTTGGCACCTCAATAGCAGCGCCCT	1599
QY	207	GAACTGCAATAGATAGCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAGTT	266
Db	1600	GAACTGCAATAGATAGCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAGTT	1659
QY	267	CAACTCTTTCAGGCTGCTCTGAGAGCTAGCCAGCTGCGCACCCCTTACCGATTTTGACCA	326
Db	1660	CAACTCTTTCAGGCTGCTCTGAGAGCTAGCCAGCTGCGCACCCCTTACCGATTTTGACCA	1719
QY	327	GGGCTGGGGCCCTATCAGTTATGCCAAGCGGGCCCGACAGCGCCCTACTGCTG	386
Db	1720	GGGCTGGGGCCCTATCAGTTATGCCAAGCGGGCCCGACAGCGCCCTACTGCTG	1779
QY	387	GCACTACCCCCCAAAACCTTGGGTATTGTCGCGCGGAAGAGTGTTGTTGTCGGGTATA	446
Db	1780	GCACTACCCCCCAAAACCTTGGGTATTGTCGCGCGGAAGAGTGTTGTTGTCGGGTATA	1839
QY	447	TTGCTTCACTCCAGCCCGTGGTGGGAACCGACAGGTGGCGCGCCCACTA	506
Db	1840	TTGCTTCACTCCAGCCCGTGGTGGGAACCGACAGGTGGCGCGCCCACTA	1899
QY	507	CAGCTGGGGTGAATGATAGCAGCGTCTTCTGCTTAACTAACATACCGCCACCGCTGGG	566
Db	1900	CAGCTGGGGTGAATGATAGCAGCGTCTTCTGCTTAACTAACATACCGCCACCGCTGGG	1959
QY	567	CAATTGGTTGCGTTGTACCTGATGAACTCACTGATTTCACTCAAGTGTCGGAGCGCC	626
Db	1960	CAATTGGTTGCGTTGTACCTGATGAACTCACTGATTTCACTCAAGTGTCGGAGCGCC	2019
QY	627	TCCTTTGTGTCATCGGAGGGCGGGCAACAACCTGCACTGCCCACTGATTTGCTTCCG	686
Db	2020	TCCTTTGTGTCATCGGAGGGCGGGCAACAACCTGCACTGCCCACTGATTTGCTTCCG	2079
QY	687	CAAGCATCCGGACCGCCACATACTCTCGTGGCGGCTCCGGTCCCTGGATCAGACCCAGTG	746
Db	2080	CAAGCATCCGGACCGCCACATACTCTCGTGGCGGCTCCGGTCCCTGGATCAGACCCAGTG	2139
QY	747	CTGTGTCGACTACCGGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACCATATT	806
Db	2140	CTGTGTCGACTACCGGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACCATATT	2199
QY	807	TAAAAATCAGGATGTACTGGGAGGGGTGCAACACAGGCTGGAAGCTGCTGCACTGGAC	866
Db	2200	TAAAAATCAGGATGTACTGGGAGGGGTGCAACACAGGCTGGAAGCTGCTGCACTGGAC	2259
QY	867	GCGGGGCGAACGTTGCGATCTGGAAGATAGGGAAGTCCGAGATC	912
Db	2260	GCGGGGCGAACGTTGCGATCTGGAAGATAGGGAAGTCCGAGATC	2305
RESULT 11			
ID	AAx26737		
XX	AAx26737 standard; DNA; 9185 BP.		
XX			
AC	AAx26737;		
XX			
DT	21-JUN-1999 (first entry)		
DE	Nucleotide sequence of the ORF of HCV1.		
XX			
KW	HCV; J7 isolate; J1 isolate; HCV1; immunoassay; asiatic strain;		
KW	diagnosis; HCV infection; blood screening; immunisation; antiviral; ss.		
XX			
OS	Hepatitis C virus.		
XX			
PN	US5871903-A.		
XX			
PD	16-FEB-1999.		
XX			
PF	08-MAY-1995; 95US-00436965.		

XX	15-SEP-1989;	89US-00408045.	
PR	21-DEC-1989;	89US-00456142.	
PR	04-JAN-1991;	91US-00637380.	
PR	02-AUG-1993;	93US-00101280.	
PR	24-FEB-1994;	94US-00201066.	
PR	03-NOV-1994;	94US-00334255.	
XX	(NAHE-) NAT INST OF HEALTH JAPAN.		
PA	(CHIR ) CHIRON CORP.		
XX	Saito I, Miyamura T;		
XX	WPI; 1999-166619/14.		
XX	Immunoassays for Asiatic strains of hepatitis C virus - for diagnosis of		
PT	infection and screening blood supplies.		
XX	Disclosure; Fig 12A-C; 43pp; English.		
XX	The present sequence represents the sequence of ORF1 of hepatitis C virus		
CC	(HCV) isolate HCV1. The specification describes new isolates of HCV, J1		
CC	and J7. J1 and J7 isolates comprise sequences which are distinct from the		
CC	prototype HCV isolates, HCV1. The specification describes immunoassays		
CC	for HCV based on antigens from Asiatic strains not cross-reactive with		
CC	HCV-1. The assays are used for diagnosis of HCV infection and to screen		
CC	donated blood. The anti-HCV antibodies are also useful therapeutically		
CC	and prophylactically (passive immunisation); in screening for antiviral		
CC	agents; for isolation, purification and identification of non-A, non-B		
CC	hepatitis virus (e.g. by affinity chromatography) and to raise anti-		
CC	idiotypic antibodies (useful for treatment or diagnosis) and to determine		
CC	immunogenic regions of the HCV antigens)		
XX	Sequence 9185 BP; 1849 A; 2792 C; 2606 G; 1938 T; 0 U; 0 Other;		
SQ			
Query Match 52.4%; Score 834.8; DB 2; Length 9185;			
Best Local Similarity 96.4%; Pred. No. 3.6e-133;			
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;			
QY	27	CTGTGTGCTGCTGTGTGGAGCAGTCTTCTGTTTCCGCCAGCGCTAGCGAAACCCACGT 86	
Db	1420	CTGGCGAAGTCTCTGTTGCTGCTCTATTTTGGCGGCTGCGAGCGGAACCCACGT 1479	
QY	87	CACCGGGGAAAGTGGCGGCCACACATGCTGTGGATTTCTTAGCTTCTCGCACGAGGCGC 146	
Db	1480	CACCGGGGAAAGTGGCGGCCACACATGCTGTGGATTTCTTAGCTTCTCGCACGAGGCGC 1539	
QY	147	CAAGCAGAACGTCCTCAGCTGATCAACACCAACGCGCAGTTGGCACCTCAATAGCAGCGCCT 206	
Db	1540	CAAGCAGAACGTCCTCAGCTGATCAACACCAACGCGCAGTTGGCACCTCAATAGCAGCGCCT 1599	
QY	207	GAACTGCAATAGATAGCTTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAGTT 266	
Db	1600	GAACTGCAATAGATAGCTTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAGTT 1659	
QY	267	CAACTCTTTCAGGCTGCTCTGAGAGCTAGCCAGCTGCGCACCCCTTACCGATTTTGACCA 326	
Db	1660	CAACTCTTTCAGGCTGCTCTGAGAGCTAGCCAGCTGCGCACCCCTTACCGATTTTGACCA 1719	
QY	327	GGGCTGGGGCCCTATCAGTTATGCCAAGCGGGCCCGACAGCGCCCTACTGCTG 386	
Db	1720	GGGCTGGGGCCCTATCAGTTATGCCAAGCGGGCCCGACAGCGCCCTACTGCTG 1779	
QY	387	GCACTACCCCCCAAAACCTTGGGTATTGTCGCGCGGAAGAGTGTTGTTGTCGGGTATA 446	
Db	1780	GCACTACCCCCCAAAACCTTGGGTATTGTCGCGCGGAAGAGTGTTGTTGTCGGGTATA 1839	
QY	447	TTGCTTCACTCCAGCCCGTGGTGGGAACCGACAGGTGGCGCGCCCACTA 506	
Db	1840	TTGCTTCACTCCAGCCCGTGGTGGGAACCGACAGGTGGCGCGCCCACTA 1899	
QY	507	CAGCTGGGGTGAATAATGATAGCAGCGTCTTCTGCTTAACTAACATACCGCCACCGCTGGG 566	

Db 1900 CAGCTGGGGTGAAATGATACCGACGCTCTTCGTCTTAAACAATACCGGCCACCGCTGGG 1959  
QY 567 CAATTGGTTTCGGTTGTACCTGATGAACCTCAACTGATTACAAAAGTGTGGGAGCGCC 626  
Db 1960 CAATTGGTTTCGGTTGTACCTGATGATCACTCAACTGATTACAAAAGTGTGGGAGCGCC 2019  
QY 627 TCCTTGTGTATCGAGGGCGGGCAACAAACCCCTGCACTGCCCCACTGATTGCTTCGG 686  
Db 2020 TCCTTGTGTATCGAGGGCGGGCAACAAACCCCTGCACTGCCCCACTGATTGCTTCGG 2079  
QY 687 CAAAGCATCCGGACGCCACATCTCTCGGTGGGGCTCCGGTCCCTGGATCACAACCCAGGTG 746  
Db 2080 CAAAGCATCCGGACGCCACATCTCTCGGTGGGGCTCCGGTCCCTGGATCACAACCCAGGTG 2139  
QY 747 CCTGGTCCGAATACCCGTTATAGGCTTTGGCAATTATCTTGATCACTCAACTACACCATATT 806  
Db 2140 CCTGGTCCGAATACCCGTTATAGGCTTTGGCAATTATCTTGATCACTCAACTACACCATATT 2199  
QY 807 TAAATCAGGATGTACGTGGGAGGGTCAACACAGGGCTGGAAGCTGCACTGGAC 866  
Db 2200 TAAATCAGGATGTACGTGGGAGGGTCAACACAGGGCTGGAAGCTGCACTGGAC 2259  
QY 867 GCGGGCGCAACGTTGGGATCTGGAGATAGGACAGGTCCTCGAGATC 912  
Db 2260 GCGGGCGCAACGTTGGGATCTGGAGATAGGACAGGTCCTCGAGATC 2305

RESULT 12

ADPF6068

ID ADF66068 standard; DNA; 9185 BP.

XX AC

XX ADF66068;

XX 12-FEB-2004 (first entry)

XX Hepatitis C virus 1 ORF nucleotide sequence.

DE Hepatitis C virus; HCV; screening; identification; non A non B hepatitis;

KW NANBH; gene; ds.

XX Hepatitis C virus.

OS Hepatitis C virus.

XX US959092-A.

XX 28-SEP-1999.

XX 08-MAY-1995; 95US-00436966.

XX 15-SEP-1989; 89US-00408045.

PR 21-DEC-1989; 89US-00456142.

PR 04-JAN-1991; 91US-00637380.

PR 02-AUG-1993; 93US-00101280.

PR 24-FEB-1994; 94US-00201066.

PR 03-NOV-1994; 94US-00334255.

XX (CHIR ) CHIRON CORP.

PA (NAHE-) NAT INST OF HEALTH JAPAN.

XX Saito I, Miyamura T;

XX WPI; 1999-570774/48.

XX Polynucleotide probes useful for screening and identifying carriers of

PT non A non B hepatitis.

XX Disclosure; Fig 12; 44pp; English.

CC The present invention describes polynucleotides sequences from Hepatitis

CC C virus (HCV) isolates J7 C/E, J1 E, J1 E/NS1, J1 NS3, and J1 NS5 or from

CC deposits BP-2593, BP2594, BP-2595, BP-2637 and BP-2638. The

CC polynucleotide sequences are useful as probes for screening and

CC identifying carriers of non A non B hepatitis (NANBH). The present

CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 9185 BP; 1849 A; 2792 C; 2606 G; 1938 T; 0 U; 0 Other;  
Query Match 52.4%; Score 834.8; DB 2; Length 9185;  
Best Local Similarity 96.4%; Pred. No. 3.6e-133;  
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 27 CTGTGTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCGCAGCGCTAGGAAACCCACCT 86  
Db 1420 CTGGGGGAAGTCTCTGGTAGTGTCTCTATTTCCCGCGCTCGACGGGAAACCCACCT 1479  
QY 87 CACCGGGGAAGTGCCTGCCCACTGTGTCTGTGATTGTGTAGCTCTCTCGCACCGAGCGC 146  
Db 1480 CACCGGGGAAGTGCCTGCCCACTGTGTCTGTGATTGTGTAGCTCTCTCGCACCGAGCGC 1539  
QY 147 CAAAGCAGACGTCAGCTGATCAACACCAACGGCAGTTGGCACCCTCAATAGCAGCGCCCT 206  
Db 1540 CAAAGCAGACGTCAGCTGATCAACACCAACGGCAGTTGGCACCCTCAATAGCAGCGCCCT 1599  
QY 207 GAACTGCAATAGTAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTT 266  
Db 1600 GAACTGCAATAGTAGCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGTT 1659  
QY 267 CAACTCTTCAGGCTGTCTGTAGAGGCTAGCCAGCTGCCAGCCCTTACCGATTTCGACCA 326  
Db 1660 CAACTCTTCAGGCTGTCTGTAGAGGCTAGCCAGCTGCCAGCCCTTACCGATTTCGACCA 1719  
QY 327 GGGCTGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGACAGCGCCCTACTGTG 386  
Db 1720 GGGCTGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCGACAGCGCCCTACTGTG 1779  
QY 387 GCACCTACCCCAAAACCTTCGGGTATTGTGCCCGGAAGAGTGTGTGGTCCGGTATA 446  
Db 1780 GCACCTACCCCAAAACCTTCGGGTATTGTGCCCGGAAGAGTGTGTGGTCCGGTATA 1839  
QY 447 TTGCTTCACTCCAGCCCCCGTGGTGGGAACGACCGACAGGTGCGGCGGCCACCTTA 506  
Db 1840 TTGCTTCACTCCAGCCCCCGTGGTGGGAACGACCGACAGGTGCGGCGGCCACCTTA 1899  
QY 507 CAGCTGGGGTGAAATGATACGGACGCTTCCTCTTAAACAATACCGAGCCACCGCTGGG 566  
Db 1900 CAGCTGGGGTGAAATGATACGGACGCTTCCTCTTAAACAATACCGAGCCACCGCTGGG 1959  
QY 567 CAATTGGTTTCGGTTGTACCTGATGAACCTCAACTGGATTTCACCAAGTGTGGGAGCGCC 626  
Db 1960 CAATTGGTTTCGGTTGTACCTGATGAACCTCAACTGGATTTCACCAAGTGTGGGAGCGCC 2019  
QY 627 TCCTTGTGTATCGAGGGCGGGCAACAAACCCCTGCACTGCCCCACTGATTGCTTCGG 686  
Db 2020 TCCTTGTGTATCGAGGGCGGGCAACAAACCCCTGCACTGCCCCACTGATTGCTTCGG 2079  
QY 687 CAAAGCATCCGGACGCCACATCTCTCGGTGGGGCTCCGGTCCCTGGATCACAACCCAGGTG 746  
Db 2080 CAAAGCATCCGGACGCCACATCTCTCGGTGGGGCTCCGGTCCCTGGATCACAACCCAGGTG 2139  
QY 747 CTGTGTGACTACCCGCTATAGGCTTTGGCAATTATCTCTGTATCACTCAACTACACCATATT 806  
Db 2140 CTGTGTGACTACCCGCTATAGGCTTTGGCAATTATCTCTGTATCACTCAACTACACCATATT 2199  
QY 807 TAAATCAGGATGTACGTGGGAGGGTCAACACAGGCTGGAAGCTGCTTCAACTGAC 866  
Db 2200 TAAATCAGGATGTACGTGGGAGGGTCAACACAGGCTGGAAGCTGCTTCAACTGAC 2259  
QY 867 GCGGGCGCAACGTTGGGATCTGGAGATAGGACAGGTCCTCGAGATC 912  
Db 2260 GCGGGCGCAACGTTGGGATCTGGAGATAGGACAGGTCCTCGAGATC 2305

RESULT 13

AAA75297

ID AAA75297 standard; cDNA; 9185 BP.

XX

AC AAA75297;

XX 15-JAN-2001 (first entry)  
XX Sense strand of HCV encoding a polyprotein.  
XX  
XX  
XX Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;  
XX viral infectivity; viral replication; ds.  
XX  
XX Hepatitis C virus.  
XX  
XX Key Location/Qualifiers  
XX 320..9184  
XX /\*tag= a  
XX /note= "partial sequence; no termination codon given"  
XX  
XX EP1034785-A2.  
XX  
XX 13-SEP-2000.  
XX  
XX 16-MAR-1990; 200EP-00109602.  
XX  
XX 17-MAR-1989; 89US-00325338.  
XX 20-APR-1989; 89US-003411334.  
XX 18-MAY-1989; 89US-00355002.  
XX 16-MAR-1990; 90EP-00302866.  
XX (CHIR ) CHIRON CORP.  
XX  
XX Houghton M, Choo Q, Kuo G;  
XX  
XX WPI, 2000-566891/53.  
XX P-FSDB; AAB18541.  
XX  
XX Novel composition comprising a hepatitis C virus antisense polynucleotide  
XX which is complementary to or corresponds to a sense strand of the virus  
XX genome, and selectively hybridizes to it.  
XX  
XX Example; Fig 17; 75pp; English.  
XX  
XX The specification describes a pharmaceutical composition which comprises  
XX a hepatitis C virus (HCV) antisense polynucleotide. The HCV is  
XX characterized by a positive stranded RNA genome which has 40% homology at  
XX the polypeptide level to a HCV polyprotein. The antisense polynucleotide  
XX binds to cellular polynucleotides which enhance and/or are required for  
XX viral infectivity, replicative ability or chronicity. The antisense  
XX polynucleotides may also be designed to bind with high specificity, to be  
XX of increased stability, to be stable and to have low toxicity. The  
XX composition also comprises an agent which causes viral RNA to be  
XX inactive. The composition is used for preventing HCV replication in a  
XX system. The present sequence represents a novel HCV cDNA sequence, which  
XX is used in the course of the invention  
XX  
XX Sequence 9185 BP; 1849 A; 2790 C; 2608 G; 1938 T; 0 U; 0 Other;  
XX  
XX Query Match 52.4%; Score 834.8; DB 3; Length 9185;  
XX Best Local Similarity 96.4%; Pred. No. 3.6e-133;  
XX Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
XX  
XX 27 CTGTGTGCTGCTGCTGTGGAGCAGTCTTCGTTTCGCCCGGCGTCCAGCGGAAACCCACGT 86  
XX 1420 CTGGGCGAAGGTCCTGCTAGTGTCTGCTATTTGGCGGCTCCAGCGGAAACCCACGT 1479  
XX  
XX 87 CACCGGGGAAGTCCCGGCACACTGTGTCTGATTTGTAGCTCTCTCGCACCGAGCGC 146  
XX 1480 CACCGGGGAAGTCCCGGCACACTGTGTCTGATTTGTAGCTCTCTCGCACCGAGCGC 1539  
XX  
XX 147 CAAGCAGAGAGTCCAGCTGATCAACCAACGACGAGTGTGGCAGCTCAATAGCAGCGCCCT 206  
XX 1540 CAAGCAGAGAGTCCAGCTGATCAACCAACGACGAGTGTGGCAGCTCAATAGCAGCGCCCT 1599  
XX  
XX 207 GAACTGCAATGATAGCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCACCACAGATT 266  
XX 1600 GAACTGCAATGATAGCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCACCACAGATT 1659  
XX

QY 267 CAACTCTTACGGCTGCTCCTGAGAGGCTAGCCAGCTGCGGAGCCCTTACCGATTTTGACCA 326  
DB 1660 CAACTCTTACGGCTGCTCCTGAGAGGCTAGCCAGCTGCGGAGCCCTTACCGATTTTGACCA 1719  
QY 327 GGGCTGGGCGCCCTATCAGTTATGCCAAGGAGCGGCCCGGACGAGCGCCCTACTACTGCTG 386  
DB 1720 GGGCTGGGCGCCCTATCAGTTATGCCAAGGAGCGGCCCGGACGAGCGCCCTACTACTGCTG 1779  
QY 387 GCACTACCCGCCCAAAACCTTTGCGGTATTTGTCGCCGGAAGAGTGTGTGTCGGGTATA 446  
DB 1780 GCACTACCCGCCCAAAACCTTTGCGGTATTTGTCGCCGGAAGAGTGTGTGTCGGGTATA 1839  
QY 447 TTGCTTCACTCCAGCGCCCGT 506  
DB 1840 TTGCTTCACTCCAGCGCCCGT 1899  
QY 507 CAGCTGGGGTGAATAATGATACGGAGCGTCTTCGTCCTTAAACAATACAGGCGCACCGCTGGG 566  
DB 1900 CAGCTGGGGTGAATAATGATACGGAGCGTCTTCGTCCTTAAACAATACAGGCGCACCGCTGGG 1959  
QY 567 CAATTGGTTTCGTTGTATCTGATGAACCTCAACTGGATTCAACAAAGTGTGCGGAGCGCC 626  
DB 1960 CAATTGGTTTCGTTGTATCTGATGAACCTCAACTGGATTCAACAAAGTGTGCGGAGCGCC 2019  
QY 627 TCCTTGTGTCACTCGGAGGGCGGCAACACACCTGCACTGCGGCACTGATTTGCTTCG 686  
DB 2020 TCCTTGTGTCACTCGGAGGGCGGCAACACACCTGCACTGCGGCACTGATTTGCTTCG 2079  
QY 687 CAAGCATCCGAGCGCCACATATCTCTCGTGGCGGTCCGCTCCCTGGATCAACCCAGGTG 746  
DB 2080 CAAGCATCCGAGCGCCACATATCTCTCGTGGCGGTCCGCTCCCTGGATCAACCCAGGTG 2139  
QY 747 CCTGTGCACTACCCGTTATAGGCTTTGGCAATTAATCCTTTGTATCAATCAATCAATCAAT 806  
DB 2140 CCTGTGCACTACCCGTTATAGGCTTTGGCAATTAATCCTTTGTATCAATCAATCAATCAAT 2199  
QY 807 TAAATCAGGATGACGTGGAGGGGTGGAACACAGCTGGAAGTGCCTGCAACTGGAC 866  
DB 2200 TAAATCAGGATGACGTGGAGGGGTGGAACACAGCTGGAAGTGCCTGCAACTGGAC 2259  
QY 867 GCGGGCGAAGCTTGGGATCTGGAGATAGGAGACAGGTCGCGAGATC 912  
DB 2260 GCGGGCGAAGCTTGGGATCTGGAGATAGGAGACAGGTCGCGAGATC 2305  
RESULT 14  
AAT12710  
ID AAT12710 standard; cDNA; 9401 BP.  
XX  
XX AAT12710;  
XX AC  
XX DT 25-MAR-2003 (revised)  
XX DT 15-MAY-1996 (first entry)  
XX  
XX Hepatitis C virus polyprotein.  
XX  
XX Non-A non-B hepatitis virus; NANBHV; HCV; antigen; detection; diagnosis;  
XX antibodies; ds.  
XX  
XX Hepatitis C virus.  
XX  
XX Key Location/Qualifiers  
XX CDS 342..9378  
XX /\*tag= a  
XX  
XX EP693687-A1.  
XX  
XX 24-JAN-1996.  
XX  
XX 03-APR-1991; 95EP-00114016.  
XX  
XX 04-APR-1990; 90US-00504352.  
XX



```
CC containing at least 8 aa. It also comprises two additional antigens from
CC two different polypeptide domains, including at least 8 aa from the NS3,
CC NS4, S or NS5 domains of the polypeptide, corresponding, respectively, to
CC aa 1050-1640; 1640-2000; 120-400 and 2000-3011 of the HCV polypeptide.
CC Alternatively, Ag1 contains at least 8 aa from the 1-122 or 9-177 aa
CC regions of the HCV polypeptide. These antigen combinations are used
CC diagnostically to detect anti-HCV antibodies, using any standard
CC immunoassay format. These antigen combinations have a broader range of
CC reactivity with antibodies than any antigen individually. (Updated on 25-
CC MAR-2003 to correct PR field.)
XX
SQ Sequence 9401 BP; 1883 A; 2860 C; 2673 G; 1985 T; 0 U; 0 Other;

Query Match      52.4%; Score 834.8; DB 2; Length 9401;
Best Local Similarity 96.4%; Pred. No. 3.6e-133;
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 27 CTGTGTGCTGCTGCTGTGGAGCAGTCTCGTTTCGCCGCGCTGCGGAAACCCACGT 86
DB 1442 CTGGGCGAAGGTCCTGGTAGTGCTGCTGCTATTTGCCGCGTGCAGCGGAAACCCACGT 1501

QY 87 CACCGGGGGAAGTCCGGCCACACACTGTCTGGATTGTTAGCCTTCCTCGCACGAGGCGC 146
DB 1502 CACCGGGGGAAGTCCGGCCACACACTGTCTGGATTGTTAGCCTTCCTCGCACGAGGCGC 1561

QY 147 CAAGCAGAACGTCAGCTGATCAACCAACGGCAGTTGGCACCTCAATAGCAGGCGCCT 206
DB 1562 CAAGCAGAACGTCAGCTGATCAACCAACGGCAGTTGGCACCTCAATAGCAGGCGCCT 1621

QY 207 GAACTGCAATGATAGCCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAGTT 266
DB 1622 GAACTGCAATGATAGCCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAGTT 1681

QY 267 CAACTCTTCAGGCTGCTCTGAGAGCTAGCAGCTGCCGACCCCTTACCGATTTTGACCA 326
DB 1682 CAACTCTTCAGGCTGCTCTGAGAGCTAGCAGCTGCCGACCCCTTACCGATTTTGACCA 1741

QY 327 GGGCTGGGGCCCTATCAGTTATGCAACCGGAAGCGGCCCGGACGAGCGCCCTACTGCTG 386
DB 1742 GGGCTGGGGCCCTATCAGTTATGCAACCGGAAGCGGCCCGGACGAGCGCCCTACTGCTG 1801

QY 387 GCACCTACCCCCCAAAACCTTGGGTATGTCGCCGGAAGAGTGTGTGGTCCGGTATA 446
DB 1802 GCACCTACCCCCCAAAACCTTGGGTATGTCGCCGGAAGAGTGTGTGGTCCGGTATA 1861

QY 447 TTGCTTTCACTCCAGCCCGCTGGTGGGAAACGACCGACAGGTGGGGCGGCCCACTTA 506
DB 1862 TTGCTTTCACTCCAGCCCGCTGGTGGGAAACGACCGACAGGTGGGGCGGCCCACTTA 1921

QY 507 CAGCTGGGGTGAATGATACGAGCTCTTCGTCCTTAACATACGAGCCACCGCTGGG 566
DB 1922 CAGCTGGGGTGAATGATACGAGCTCTTCGTCCTTAACATACGAGCCACCGCTGGG 1981

QY 567 CAATTGGTTTCGGTTGCTGATGAACCTCAACTGGATTCAACAAAGTGTGGGAGCGCC 626
DB 1982 CAATTGGTTTCGGTTGCTGATGAACCTCAACTGGATTCAACAAAGTGTGGGAGCGCC 2041

QY 627 TCCTTGTGTATCGGAGGGCGGGCAACACACCCCTGCACTGCCCCACTGATTGCTTCG 686
DB 2042 TCCTTGTGTATCGGAGGGCGGGCAACACACCCCTGCACTGCCCCACTGATTGCTTCG 2101

QY 687 CAAGCATCCGGAGCGGCACATATCTCTCGGTGGGCTCCGGTCCCTGGATCACACCCAGGTG 746
DB 2102 CAAGCATCCGGAGCGGCACATATCTCTCGGTGGGCTCCGGTCCCTGGATCACACCCAGGTG 2161

QY 747 CCTGGTTCGACTACCCGTATAGGCTTTGGCATATCTCTGTACCATCAACTACACCATATT 806
DB 2162 CCTGGTTCGACTACCCGTATAGGCTTTGGCATATCTCTGTACCATCAACTACACCATATT 2221

QY 807 TAAATCAGGATGATAGTGGGAGGGGTGGAACACAGGCTGGAAGCTGCCTGCAACTGGAC 866
DB 2222 TAAATCAGGATGATAGTGGGAGGGGTGGAACACAGGCTGGAAGCTGCCTGCAACTGGAC 2281
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QY 867 GCGGGGCGAAACGTTGCGATCTGGAAGATAGGGACAGGTCCGAGATC 912
DB 2282 GCGGGGCGAAACGTTGCGATCTGGAAGACAGGGACAGGTCCGAGCTC 2327

Search completed: April 14, 2005, 23:14:07
Job time : 900 secs
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Db 2292 TCCGACCCCTTACCGATTTTGACACAGGCTGGGCCCTATCAGTTATGCCAACCGAAGC 2351  
QY 361 GGGCCCGACAGCGCCCTACTGCTGGCACTACCCCCCAAAACCTTGGGATTTGTGCC 420  
Db 2352 GGGCCCGACAGCGCCCTACTGCTGGCACTACCCCCCAAAACCTTGGGATTTGTGCC 2411  
QY 421 GCGAAGAGTGTGTGGTCCGGTATATTGCTTCACTCCAGCCCGTGTGTGGGAAG 480  
Db 2412 GCGAAGAGTGTGTGGTCCGGTATATTGCTTCACTCCAGCCCGTGTGTGGGAAG 2471  
QY 481 ACCGACAGTCCGGCGGCCACCTACAGCTCGGGTGAAAATGATACGACGCTTTCGTC 540  
Db 2472 ACCGACAGTCCGGCGGCCACCTACAGCTCGGGTGAAAATGATACGACGCTTTCGTC 2531  
QY 541 CTTAAACAATACCAGGCCACCGCTGGGCAATTTGGTTCGGTTGTACCTGGATGAACCTCAACT 600  
Db 2532 CTTAAACAATACCAGGCCACCGCTGGGCAATTTGGTTCGGTTGTACCTGGATGAACCTCAACT 2591  
QY 601 GGATTACCAAAAGTGTGGAGGCGCTCCTTGTGTATCGGAGGGCGGGCAACACACC 660  
Db 2592 GGATTACCAAAAGTGTGGAGGCGCTCCTTGTGTATCGGAGGGCGGGCAACACACC 2651  
QY 661 CTGCACTGCCCACTGATTGCTTCGCAAGCATCCGACGCCACATACCTCTCGGTGCGGC 720  
Db 2652 CTGCACTGCCCACTGATTGCTTCGCAAGCATCCGACGCCACATACCTCTCGGTGCGGC 2711  
QY 721 TCCGGTCCCTGGATCACACCCAGGTGCTGGTGCAGTACCCGTATAGGCTTTGGCATTAT 780  
Db 2712 TCCGGTCCCTGGATCACACCCAGGTGCTGGTGCAGTACCCGTATAGGCTTTGGCATTAT 2771  
QY 781 CCTTGTACCATCAACTACACCATATTTAAATCAGGATGTAGTGGAGGGGTGCAACAC 840  
Db 2772 CCTTGTACCATCAACTACACCATATTTAAATCAGGATGTAGTGGAGGGGTGCAACAC 2831  
QY 841 AGGCTGGAAGTCCCTGCAACTGGACGGGGCGAACGTTGCGATCTGGAAGATAGGGAC 900  
Db 2832 AGGCTGGAAGTCCCTGCAACTGGACGGGGCGAACGTTGCGATCTGGAAGATAGGGAC 2891  
QY 901 AGGCTCGAGATCGATATGAGAACATCACATCAGGATTCCTAGGACCCCTGCTCGTGTGA 960  
Db 2892 AGGCTCGAGATCGATATGAGAACATCACATCAGGATTCCTAGGACCCCTGCTCGTGTGA 2951  
QY 961 CAGGCGGGGTTTTCTTGTGTGACAGAATCTTCAATACCGAGAGTCTAGACTCGTGG 1020  
Db 2952 CAGGCGGGGTTTTCTTGTGTGACAGAATCTTCAATACCGAGAGTCTAGACTCGTGG 3011  
QY 1021 TGGACTTCTCAATTTCTAGGGGATCTCCGCTGTGTTGGCCAAATTCGCAAGTCC 1080  
Db 3012 TGGACTTCTCAATTTCTAGGGGATCTCCGCTGTGTTGGCCAAATTCGCAAGTCC 3071  
QY 1081 CCAACTCCAATCACTCAACAACTCTGCTCCTCAATTTGTCTGGTTATCGCTGGATG 1140  
Db 3072 CCAACTCCAATCACTCAACAACTCTGCTCCTCAATTTGTCTGGTTATCGCTGGATG 3131  
QY 1141 TGTCTCGGGGTTTTATCATATTCCTTTCATCCTGCTGCTATGCCTCATCTCTTATTG 1200  
Db 3132 TGTCTCGGGGTTTTATCATATTCCTTTCATCCTGCTGCTATGCCTCATCTCTTATTG 3191  
QY 1201 GTTCTTCTGGATTATCAAGGTATGTTGCCGTTTGTCTTAATTCAGGATCAACAA 1260  
Db 3192 GTTCTTCTGGATTATCAAGGTATGTTGCCGTTTGTCTTAATTCAGGATCAACAA 3251  
QY 1261 ACCAGTACGGGACCATGCAAAACCTGCAAGTCTCTGCTCAAGGCAACTCTATGTTTCCC 1320  
Db 3252 ACCAGTACGGGACCATGCAAAACCTGCAAGTCTCTGCTCAAGGCAACTCTATGTTTCCC 3311  
QY 1321 TCATGTTGTGTACAAAACCTAGGATGGAATTCACCTGTATTCGGATCCCATCGTCC 1380  
Db 3312 TCATGTTGTGTACAAAACCTAGGATGGAATTCACCTGTATTCGGATCCCATCGTCC 3371  
QY 1381 TGGGCTTTTCGAAAATACCTATGGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTA 1440

Db 3372 TGGGCTTTTCGAAAATACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTA 3431  
QY 1441 CTAGTGCCATTTGTTCACTGTTTCTAGGCTTTTCCCACTGTTTGGCTTTTCACTATA 1500  
Db 3432 CTAGTGCCATTTGTTCACTGTTTCTAGGCTTTTCCCACTGTTTGGCTTTTCACTATA 3491  
QY 1501 TGGATGATGTGTATTGGGGCCAAAGTCTGTACACATCGTGAGTCCCTTTTATACCGCTG 1560  
Db 3492 TGGATGATGTGTATTGGGGCCAAAGTCTGTACACATCGTGAGTCCCTTTTATACCGCTG 3551  
QY 1561 TTACCAATTTTCTTTTGTCTCTGGGTATACATT 1593  
Db 3552 TTACCAATTTTCTTTTGTCTCTGGGTATACATT 3584

RESULT 2  
US-09-693-596-3  
; Sequence 3, Application US/09693596  
; Patent No. 6521423  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Michael  
; APPLICANT: Choo, Qui-lim  
; APPLICANT: Abignani, Sergio  
; APPLICANT: Chien, David  
; APPLICANT: Selby, Mark  
; APPLICANT: Glazer, Edward  
; TITLE OF INVENTION: Intracellular Production of Hepatitis C E1 and E2  
; FILE OF INVENTION: Truncated Polypeptides  
; FILE REFERENCE: 1378.002  
; CURRENT APPLICATION NUMBER: US/09/693,596  
; CURRENT FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/073,406  
; PRIOR FILING DATE: 1998-05-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1989  
; TYPE: DNA  
; ORGANISM: Hepatitis C virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1989)  
US-09-693-596-3

Query Match 52.5%; Score 836.4; DB 4; Length 1989;  
Best Local Similarity 96.5%; Pred. No. 2.5e-259;  
Matches 855; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 27 CTGTGCTGCTGCTGTGTGGAGCAGTCTTCTGTTCCGCCAGCGCTAGCGAAACCCACCGT 86  
Db 12 CTGGCGGAAGTCTCTGGTAGTCTGCTGCTATTTGCGGCGTGGACGGGAAACCCACCGT 71  
QY 87 CACCGGGGAAGTGC CGGCCACACATGTGTCTGGAATTTGTTAGCTCTCTCGCACCGGCGC 146  
Db 72 CACCGGGGAAGTGC CGGCCACACATGTGTCTGGAATTTGTTAGCTCTCTCGCACCGGCGC 131  
QY 147 CAGCAGAACGTCAGCTGATCAACCAACGGCAGTTGGCAGCTCAATAGCAGCGCCCT 206  
Db 132 CAGCAGAACGTCAGCTGATCAACCAACGGCAGTTGGCAGCTCAATAGCAGCGCCCT 191  
QY 207 GAACTGCAATGATAGCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAGTT 266  
Db 192 GAACTGCAATGATAGCTCAACACCGGCTGTTGGCAGGGCTTTTCTATCACCACAAGTT 251  
QY 267 CAACTCTTCAGGCTGCTCTGAGAGGCTAGCCAGTGTCCGACCCCTTACCGATTTTGACCA 326  
Db 252 CAACTCTTCAGGCTGCTCTGAGAGGCTAGCCAGTGTCCGACCCCTTACCGATTTTGACCA 311  
QY 327 GGGCTGGGGCCCTATCAGTTATGCCAAGGAGCGGCCCGCCAGCGCCCTACTGCTG 386  
Db 312 GGGCTGGGGCCCTATCAGTTATGCCAAGGAGCGGCCCGCCAGCGCCCTACTGCTG 371  
QY 387 GCACTACCCCCCAAAACCTTGGGTTATTGTGCGGATTTGTGCGCGAAGAGTGTGTGTCGGGTATA 446



QY 747 CTTGTCGACTACCCGTATAGCTTTGGCAATTATCTTGTACCATCAACTACACCATATT 806  
 DB 805 CTTGTCGACTACCCGTATAGCTTTGGCAATTATCTTGTACCATCAACTACACCATATT 864  
 QY 807 TAAATCAGGATGTACGTGGAGGGTTCGAAACACAGGCTGGAAGCTGCCTGCAACTGGAC 866  
 DB 865 TAAATCAGGATGTACGTGGAGGGTTCGAAACACAGGCTGGAAGCTGCCTGCAACTGGAC 924  
 QY 867 GCGGGCGAAGCTTGCAGTCTCGAAGATAGGACAGGTCGAGATC 912  
 DB 925 GCGGGCGAAGCTTGCAGTCTCGAAGATAGGACAGGTCGAGATC 970

RESULT 4  
 US-08-325-630-12  
 ; Sequence 12, Application US/08325630  
 ; Patent No. 5750331  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MIYAMURA, TATSUO  
 ; APPLICANT: SAITO, IZUMU  
 ; APPLICANT: HARADA, SHIZUKO  
 ; APPLICANT: HONDA, YOSHIKAZU  
 ; TITLE OF INVENTION: DIAGNOSTIC REAGENT FOR HEPATITIS C  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
 ; ADDRESSEE: P.C.  
 ; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
 ; CITY: Arlington  
 ; STATE: Virginia  
 ; COUNTRY: U.S.A.  
 ; ZIP: 22202

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/325,630  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/956,993  
 FILING DATE: 06-OCT-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Oblon, No. 5750331man P.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 4667-001-0  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703) 413-3000  
 TELEFAX: (703) 413-2220  
 TELEX: 24855 OPAT UR  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1207 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Hepatitis C virus  
 IMMEDIATE SOURCE:  
 CLONE: HCV1  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 2..1207  
 US-08-325-630-12

Query Match 52.4%; Score 834.8; DB 1; Length 1207;  
 Best Local Similarity 96.4%; Pred. No. 6e-259;  
 Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 27 CTGTCGTCTGCTGTGGAGAGTCTTCTGTTTCCGCCAGCGCTAGCGAAACCCACGT 86  
 DB 85 TTGGCGGAAGGTCCTGGTAGTCTGCTGCTATTTCCCGCGCTCGAGCGGGAACCCACGT 144  
 QY 87 CACCGGGGAAGTGCCTGGCCACACATGTCGTGATTTGTTAGCTTCTCTCGCACCGAGCGC 146  
 DB 145 CACCGGGGAAGTGCCTGGCCACACATGTCGTGATTTGTTAGCTTCTCTCGCACCGAGCGC 204  
 QY 147 CAAGCAGAACCTTCAGCTGATCAACACCAACGAGAGTGGCACTCAATAGACGCGCCCT 206  
 DB 205 CAAGCAGAACCTTCAGCTGATCAACACCAACGAGAGTGGCACTCAATAGACGCGCCCT 264  
 QY 207 GAACTGCAATGATAGCTTCAACACCGGCTGGTGGCAGGGCTTTCTATCACCACAAGTT 266  
 DB 265 GAACTGCAATGATAGCTTCAACACCGGCTGGTGGCAGGGCTTTCTATCACCACAAGTT 324  
 QY 267 CAACTCTTTCAGGCTGCTCTGAGAGCTAGCCAGCTGCGGACCCCTTACCGATTTTGACCA 326  
 DB 325 CAACTCTTTCAGGCTGCTCTGAGAGCTAGCCAGCTGCGGACCCCTTACCGATTTTGACCA 384  
 QY 327 GGGCTGGGGCCCTATCAGTTATGCAACGGAAGCGGCCCGGACGAGCGCCCTACTGCTG 386  
 DB 385 GGGCTGGGGCCCTATCAGTTATGCAACGGAAGCGGCCCGGACGAGCGCCCTACTGCTG 444  
 QY 387 GCACCTACCCCGCAAAACCTTGGGTATTTGTCGCCGGAAGAGTGTGTGTCCTCGGTATA 446  
 DB 445 GCACCTACCCCGCAAAACCTTGGGTATTTGTCGCCGGAAGAGTGTGTGTCCTCGGTATA 504  
 QY 447 TTGCTTTCACCTCCAGCGCCCGTGGTGGGAACGACCGACAGGTCGGGCGCCCGCACCTTA 506  
 DB 505 TTGCTTTCACCTCCAGCGCCCGTGGTGGGAACGACCGACAGGTCGGGCGCCCGCACCTTA 564  
 QY 507 CAGCTGGGGTGAATATGATACGGAAGTCTTCTGCTTAACTAACATACAGGCGCCCGTGGG 566  
 DB 565 CAGCTGGGGTGAATATGATACGGAAGTCTTCTGCTTAACTAACATACAGGCGCCCGTGGG 624  
 QY 567 CAATTTGGTTCGGTCTGATGATCAACTCAACTGATTTACCAAAAGTGTGCGGAGCGCC 626  
 DB 625 CAATTTGGTTCGGTCTGATGATCAACTCAACTGATTTACCAAAAGTGTGCGGAGCGCC 684  
 QY 627 TCCTTTGTGTCATCGGAGGGCGGCAACCAACCCCTGCACTGCCCGCTGATTTGCTTCCG 686  
 DB 685 TCCTTTGTGTCATCGGAGGGCGGCAACCAACCCCTGCACTGCCCGCTGATTTGCTTCCG 744  
 QY 687 CAAGCATCGGAGCGCCACATCTCTGGTGGGCTCCGGTCCCTGATCACACCGAGGTG 746  
 DB 745 CAAGCATCGGAGCGCCACATCTCTGGTGGGCTCCGGTCCCTGATCACACCGAGGTG 804  
 QY 747 CCTGCTGACTACCCGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACACCATATT 806  
 DB 805 CCTGCTGACTACCCGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACACCATATT 864  
 QY 807 TAAATCAGGATGTACGTGGAGGGTTCGAAACACAGGCTGGAAGCTGCTGCAACTGGAC 866  
 DB 865 TAAATCAGGATGTACGTGGAGGGTTCGAAACACAGGCTGGAAGCTGCTGCAACTGGAC 924  
 QY 867 GCGGGCGAAGCTTGCAGTCTCGAAGATAGGACAGGTCGAGATC 912  
 DB 925 GCGGGCGAAGCTTGCAGTCTCGAAGATAGGACAGGTCGAGATC 970

RESULT 5  
 US-08-444-818-88  
 ; Sequence 88, Application US/08444818  
 ; Patent No. 6150087  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chien, David Y.  
 ; APPLICANT: Rutter, William J.  
 ; TITLE OF INVENTION: NANV Diagnostics and Vaccines  
 ; NUMBER OF SEQUENCES: 777  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Chiron Corporation  
 ; STREET: 4560 Horton Street

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; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..8316
; US-08-444-818-88

Query Match          52.4%; Score 834.8; DB 3; Length 8316;
Best Local Similarity 96.4%; Pred. No. 2.1e-258;
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 27 CTGTGCTGCTGCTGTGTGAGCAGCTCTTCGTTTCGCCAGCGCTAGCGAACCACCGT 86
DB 759 CTTGGCGAAGTCTGTGTAGTGTCTGCTGCTATTTCGCCGCTGACGCGGAACCCACGT 818

QY 87 CACCGGGGAAGTCCCGGCCACACTGTGTCTGGATTGTAGCTCTCTCGCACCGCGC 146
DB 819 CACCGGGGAAGTCCCGGCCACACTGTGTCTGGATTGTAGCTCTCTCGCACCGCGC 878

QY 147 CAAGCAGACGCTCCAGCTGATCAACACCAACCGCAGTTGGCAGCTCAATAGCAGCGCCT 206
DB 879 CAAGCAGACGCTCCAGCTGATCAACACCAACCGCAGTTGGCAGCTCAATAGCAGCGCCT 938

QY 207 GAATCGAATGATAGCTCAACACCGCTGTTGGCAGGCTTTCTATCACCACCAAGTT 266
DB 939 GAATCGAATGATAGCTCAACACCGCTGTTGGCAGGCTTTCTATCACCACCAAGTT 998

QY 267 CAATCTCTCAGGCTGCTCCTGAGAGGCTAGCAGCTGCCGCCCTTACCAGTTTGACCA 326
DB 999 CAATCTCTCAGGCTGCTCCTGAGAGGCTAGCAGCTGCCGCCCTTACCAGTTTGACCA 1058

QY 327 GGCGTGGGCGCTTATCAGTTTATGCCAAGCGCGCGCCGACAGCGCGCCCTTACTGCTG 386
DB 1059 GGCGTGGGCGCTTATCAGTTTATGCCAAGCGCGCGCCGACAGCGCGCCCTTACTGCTG 1118

QY 387 GCATACCCCGGAAACCTTGGGTTATGTCGCGGAGAGTGTTGGTCCGGTATA 446
DB 1119 GCATACCCCGGAAACCTTGGGTTATGTCGCGGAGAGTGTTGGTCCGGTATA 1178

QY 447 TTGCTTCACTCCAGCGCCGCTGTGTGGGAAACGACGACAGCTCGCGCGCGCCACCTA 506
DB 1179 TTGCTTCACTCCAGCGCCGCTGTGTGGGAAACGACGACAGCTCGCGCGCGCCACCTA 1238

QY 507 CAGCTGGGTGAAATGATACGACGCTTCTGCTTAAACAATACGAGCCACCGTGGG 566
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DB 1239 CAGCTGGGTGAAATGATACGACGCTTCTGCTTAAACAATACGAGCCACCGCTGGG 1298
QY 567 CAATTGTTGCGTTGTACCTGGATGAACCACTGGATTTCACCAAAAGTGTCCGAGCGCC 626
DB 1299 CAATTGTTGCGTTGTACCTGGATGAACCACTGGATTTCACCAAAAGTGTCCGAGCGCC 1358
QY 627 TCCTTGTGTATCGGAGGGCGGGCAACAACACCTGCACTGCCCACTGATTGCTTCCG 686
DB 1359 TCCTTGTGTATCGGAGGGCGGGCAACAACACCTGCACTGCCCACTGATTGCTTCCG 1418
QY 687 CAAGCATCCGAGCGCCACATACCTCTCGTCCGGCTCCGTCCTTGGATCACACCCAGTG 746
DB 1419 CAAGCATCCGAGCGCCACATACCTCTCGTCCGGCTCCGTCCTTGGATCACACCCAGTG 1478
QY 747 CTTGCTCGACTACCCGCTATAGGCTTTTGGCATTTATCTTTGATACCATCAACCTACCATATT 806
DB 1479 CTTGCTCGACTACCCGCTATAGGCTTTTGGCATTTATCTTTGATACCATCAACCTACCATATT 1538
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DB 1539 TAAATCAGGATGTACGTGGAGGGTTCGAACACAGGCTGGAAGCTGCTGCAACTGGAC 1598
QY 867 GCGGGCGGAACGTTGCGATCTGGAAGATAGGAGCAGGTCCGAGATC 912
DB 1599 GCGGGCGGAACGTTGCGATCTGGAAGATAGGAGCAGGTCCGAGATC 1644

RESULT 6
US-08-444-818-122
; Sequence 122, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Ruter, William J.
; TITLE OF INVENTION: NANEV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9185 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-444-818-122

Query Match          52.4%; Score 834.8; DB 3; Length 9185;
Best Local Similarity 96.4%; Pred. No. 2.3e-258;
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Qy	87	CACCGGGGAAGTGC CGGCACACTGTGTCTGTGATTTGTTAGCTCTCTCGACACAGGCGC	146						
Db	1480	CACCGGGGAAGTGC CGGCACACTGTGTCTGTGATTTGTTAGCTCTCTCGACACAGGCGC	1539						
Qy	147	CAAGCAGACGTCACAGCTGATCAACACCAAGGCGAGTTGGACCTCAATAGCAGGCGCT	206						
Db	1540	CAAGCAGACGTCACAGCTGATCAACACCAAGGCGAGTTGGACCTCAATAGCAGGCGCT	1599						
Qy	207	GAACCTCAATATAGACCTCAACACCGGCTGGTGGCAGGCGTTTCTATCACACAAAGTT	266						
Db	1600	GAACCTCAATATAGACCTCAACACCGGCTGGTGGCAGGCGTTTCTATCACACAAAGTT	1659						
Qy	267	CAACTCTTCAGGCTGCTCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCAGTTTGAACCA	326						
Db	1660	CAACTCTTCAGGCTGCTCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCAGTTTGAACCA	1719						
Qy	327	GGGCTGGGGCCCTATCAGTTATGCCAACGAAGCGGCGCCCGACAGCGCCCTACTGCTG	386						
Db	1720	GGGCTGGGGCCCTATCAGTTATGCCAACGAAGCGGCGCCCGACAGCGCCCTACTGCTG	1779						
Qy	387	GCACCTACCCCCAAAACCTTGCGGTATTGTGCCCGCAAGAGTGTGTGGTCCGGTATA	446						
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Qy	447	TTGCTTCACTCCCAAGCCCGTGTGTGTGGAAACGACAGAGTTCGGCGCGGCCACCTA	506						
Db	1840	TTGCTTCACTCCCAAGCCCGTGTGTGTGGAAACGACAGAGTTCGGCGCGGCCACCTA	1899						
Qy	507	CAGCTGGGTGAAAATGATACGAGCGTCTTCGCTTAACAATACAGGCGCAGCGCTGGG	566						
Db	1900	CAGCTGGGTGAAAATGATACGAGCGTCTTCGCTTAACAATACAGGCGCAGCGCTGGG	1959						
Qy	567	CAATTGGTTGCGTTGTACCTGGATGAATCAACTGGAACTCAACAAAGTGTGCGGAGCGCC	626						
Db	1960	CAATTGGTTGCGTTGTACCTGGATGAATCAACTGGAACTCAACAAAGTGTGCGGAGCGCC	2019						
Qy	627	TCCTTTGTGTCATCGGAGGGCGGGCAACACACCCCTGCACCTGCCCGCCACTGATTCCTCCG	686						
Db	2020	TCCTTTGTGTCATCGGAGGGCGGGCAACACACCCCTGCACCTGCCCGCCACTGATTCCTCCG	2079						
Qy	687	CAAGCATCCGGAACGCAACATACTCTCGGTGCGGTCCGGTCCCTGTGATCAACCCAGGTG	746						
Db	2080	CAAGCATCCGGAACGCAACATACTCTCGGTGCGGTCCGGTCCCTGTGATCAACCCAGGTG	2139						
Qy	747	CCTGGTCGACTACCGGTATAGGCTTTGGCATTATCCTTGTAACCATCACTACACCATATT	806						
Db	2140	CCTGGTCGACTACCGGTATAGGCTTTGGCATTATCCTTGTAACCATCACTACACCATATT	2199						
Qy	807	TAAATCAGGATGTACGTGGAGGGGTGCAACACAGGCTGGAAGCTGCCTGCAACTGGAC	866						
Db	2200	TAAATCAGGATGTACGTGGAGGGGTGCAACACAGGCTGGAAGCTGCCTGCAACTGGAC	2259						
Qy	867	GCGGGGCGAAGCTTGCATCTGGAAGATAGGACAGGTCCGAGATC	912						
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## RESULT 7

US-08-444-818-123/c  
Sequence 123, Application US/08444818  
Patent No. 6150087  
GENERAL INFORMATION:  
APPLICANT: Chien, David Y.  
APPLICANT: Rutter, William J.  
TITLE OF INVENTION: NANBV Diagnostics and Vaccines  
NUMBER OF SEQUENCES: 777  
CORRESPONDENCE ADDRESS:







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; OTHER INFORMATION: can also be Thr."
; FEATURE:
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; LOCATION: 4167_feature
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Leu."
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; OTHER INFORMATION: /note= "This amino acid position
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; OTHER INFORMATION: /note= "This amino acid position
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; LOCATION: 6183_
; OTHER INFORMATION: /note= "This amino acid position
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; LOCATION: 9327
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Pro."
US-07-910-760-9

Query Match 52.4%; Score 834.8; DB 1; Length 9401;
Best Local Similarity 96.4%; Pred. No. 2.3e-258;
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 27 CTGTGTGCTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCGCAGCGCTAGGAAACCCACGT 86
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QY 87 CACCGGGGGAAGTGGCGGCCACACACTGTGTCTGATTGTTAGCTCTCTCGCACGAGCGC 146
DB 1502 CACCGGGGGAAGTGGCGGCCACACACTGTGTCTGATTGTTAGCTCTCTCGCACGAGCGC 1561
QY 147 CAAGCAGAACGTCCTGAGCTGATCAACCAACCGGAGTGTGGCACCTCAATAGCACGCCCT 206
DB 1562 CAAGCAGAACGTCCTGAGCTGATCAACCAACCGGAGTGTGGCACCTCAATAGCACGCCCT 1621
QY 207 GAACCTGCAATGATAGCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCACCACAAGTT 266
DB 1622 GAACCTGCAATGATAGCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCACCACAAGTT 1681
QY 267 CAACTCTTCAGGCTGTCTCTGAGAGCTAGCCAGCTGCCGACCCCTTTACCGATTTCACCA 326
DB 1682 CAACTCTTCAGGCTGTCTCTGAGAGCTAGCCAGCTGCCGACCCCTTTACCGATTTCACCA 1741
QY 327 GGGCTGGGGCCCTATCAGTTATGCCAAGGAGCGGCCCGCCAGCGCCCTTACTGTG 386
DB 1742 GGGCTGGGGCCCTATCAGTTATGCCAAGGAGCGGCCCGCCAGCGCCCTTACTGTG 1801
QY 387 GCACCTACCCCGCAAAACCTTCGGGTATTTGTGCCCGGGAAGAGTGTGTGTCGGTATA 446
DB 1802 GCACCTACCCCGCAAAACCTTCGGGTATTTGTGCCCGGGAAGAGTGTGTGTCGGTATA 1861
QY 447 TTGCTTCACTCCCGAGCCCGTGGTGGGAACGACCGAGCTGGGGCGGCCACCTA 506
DB 1862 TTGCTTCACTCCCGAGCCCGTGGTGGGAACGACCGAGCTGGGGCGGCCACCTA 1921
QY 507 CAGCTGGGGTGAATAATGATAGCAGCTCTTCGCTCTTAAACAACAGGCCACCGCTGGG 566
DB 1922 CAGCTGGGGTGAATAATGATAGCAGCTCTTCGCTCTTAAACAACAGGCCACCGCTGGG 1981
QY 567 CAAATTGGTTCGGTTGTACTGTGATGAACTCAACTGGATTCAACAAGTGTGGGAGCGCC 626
DB 1982 CAAATTGGTTCGGTTGTACTGTGATGAACTCAACTGGATTCAACAAGTGTGGGAGCGCC 2041
QY 627 TCCTTTGTCTATCGGAGGGGGGCAACAACACCTGCACTGCCACCTGATTGCTTCG 686
DB 2042 TCCTTTGTCTATCGGAGGGGGGCAACAACACCTGCACTGCCACCTGATTGCTTCG 2101
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DB 2162 CCTGTGCACTACCGGTATAGCTTTGGCATTTATCTTTGTACCATCAACTACCATATT 2221
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DB 2222 TAAATCAGGATGTACGTGGGAGGGGTGGAACACAGGCTGGAAGTCCCTGCACTGGAC 2281
QY 867 GCGGGGCAACGTTGCGATCTGGAAGATAGGAGACAGGTCCGAGATC 912
DB 2282 GCGGGGCAACGTTGCGATCTGGAAGACAGGACAGGTCCGAGATC 2327

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RESULT 11  
 US-08-440-519-9  
 ; Sequence 9, Application US/08440519

Patent No. 5712087  
GENERAL INFORMATION:  
APPLICANT: Houghton, Michael  
APPLICANT: Choo, Qui-Lim  
APPLICANT: Kuo, George  
TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)  
TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: P.O. Box 8097 (Int. Prop. R-440)  
CITY: Emeryville  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,519  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/910,760  
FILING DATE: 07-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Blackburn Esq., Robert P.  
REGISTRATION NUMBER: 30,447  
REFERENCE/DOCKET NUMBER: 0101.002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2702  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9401 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 342..9374  
FEATURE:  
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LOCATION: 366  
OTHER INFORMATION: /note= "This amino acid position  
OTHER INFORMATION: can also be Arg."  
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NAME/KEY: misc\_feature  
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; US-08-440-519-9

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Best Local Similarity 96.4%; Pred. No. 2.3e-258;
Matches 854; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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QY 327 GGGCTGGGCGCTTATCAGTTATGCCAAGCGAGCGCGCCCGACCGCGCCCTACTGCTG 386
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QY 687 CAAGCATCCGAGCGGCACATCTCTCGGTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 746
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Db 2222 TAAATCAGAGTGTACGTGGAGGGGTGCAACACAGGCTGGAAGCTGCTGCAACTGGAC 2281
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RESULT 12
US-08-440-549-9
; Sequence 9, Application US/08440549
; Patent No. 6312889
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
; TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: P.O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,549
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,760
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Bq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9401 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
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Job time : 376 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 14, 2005, 23:14:12 ; Search time 964 Seconds  
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Searched: 5622541 seqs, 303335566 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	834.8	52.4	9379	9	US-09-916-359-1
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4	833.2	52.3	1914	15	US-10-187-257-3
5	833.2	52.3	1914	16	US-10-265-083-1
6	745.2	46.8	9646	9	US-09-742-659-3
7	745.2	46.8	9646	9	US-09-238-076-1
8	745.2	46.8	9646	10	US-09-995-937-1
9	745.2	46.8	9646	10	US-09-917-563-1
10	745.2	46.8	12980	9	US-09-238-076-5
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13	742	46.6	1845	17	US-10-365-620-73	Sequence 73, Appli
14	742	46.6	1845	19	US-10-912-969-75	Sequence 75, Appli
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16	742	46.6	2517	19	US-10-912-969-77	Sequence 77, Appli
17	742	46.6	2517	19	US-10-913-171-48	Sequence 48, Appli
18	742	46.6	9599	17	US-10-189-359-13	Sequence 13, Appli
19	742	46.6	10803	9	US-09-747-419-17	Sequence 17, Appli
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22	740.4	46.5	9416	13	US-10-104-966-13	Sequence 13, Appli
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28	738.8	46.4	9416	10	US-09-917-563-19	Sequence 19, Appli
29	738.8	46.4	9422	18	US-10-475-989-2	Sequence 2, Appli
30	738	46.3	1266	19	US-10-912-969-71	Sequence 71, Appli
31	738	46.3	1938	17	US-10-365-620-71	Sequence 71, Appli
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36	678	42.6	1696	15	US-10-267-922-15	Sequence 15, Appli
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38	676.2	42.4	1365	17	US-10-365-620-33	Sequence 33, Appli
39	676.2	42.4	1365	19	US-10-912-969-37	Sequence 37, Appli
40	676.2	42.4	2037	17	US-10-365-620-28	Sequence 28, Appli
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45	674.8	42.4	3221	19	US-10-856-355-29	Sequence 29, Appli

## ALIGNMENTS

RESULT 1

US-10-371-040-3

; Sequence 3, Application US/10371040

; Publication No. US20040001854A1

; GENERAL INFORMATION:

; APPLICANT: Houghton, Michael

; APPLICANT: Choo, Qui-Lim

; APPLICANT: Abrignani, Sergio

; APPLICANT: Chien, David

; APPLICANT: Selby, Mark

; TITLE OF INVENTION: Intracellular Production of Hepatitis C E1 and E2

; TITLE OF INVENTION: Truncated Polypeptides

; FILE REFERENCE: 1378.002

; CURRENT APPLICATION NUMBER: US/10371,040

; CURRENT FILING DATE: 2003-02-18

; PRIOR APPLICATION NUMBER: US/09/073,406

; PRIOR FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/045,675

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 1989

; TYPE: DNA

; ORGANISM: Hepatitis C virus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1989)

US-10-371-040-3

Query Match 52.5%; Score 836.4; DB 17; Length 1989;  
Best Local Similarity 96.5%; Pred. No. 9.2e+268;  
Matches 855; Conservative 0; Mismatches 31; Indels 0; Gaps 0;





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QY 327 GGGCTGGGCGCCCTATCAGTTATGCCAAACGGAAGCGCGCCGACCGCGCCCTACTGCTG 386
DB 885 GGGCTGGGCGCCCTATCAGTTATGCCAAACGGAAGCGCGCCGACCGCGCCCTACTGCTG 944
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RESULT 5
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; Sequence 1, Application US/10265083
; Publication No. US20030170273A1
; GENERAL INFORMATION:
; APPLICANT: O'HAGAN, Derek
; APPLICANT: VALIANTE, Nicholas
; TITLE OF INVENTION: ADJUVANT COMPOSITIONS
; FILE REFERENCE: 2302-18357.30
; CURRENT APPLICATION NUMBER: US/10/265,083
; CURRENT FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1911)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HCV-1 E1/E2/p7
; OTHER INFORMATION: region
US-10-265-083-1

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Query Match 52.3%; Score 833.2; DB 16; Length 1914;
Best Local Similarity 96.3%; Pred. No. 1.1e-266;
Matches 853; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 27 CTGTGTGCTGCTGCTGTGTGGAGCAGTCTTTCGTTTCGCCCGAGCGCTAGCGAAACCCACGT 86
DB 585 CTGGCGGAAGGTCCTGTGTAGTGTGCTGTGCTATTTCGCGGGGTGACGCGGAAACCCACGT 644

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QY 87 CACCGGGGAGTGC CGGCCACAC TGTGCTG GATTGTTAGCTCTCTCGCACCGAGCGC 146
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QY 267 CAACTCTTCAGGCTG CTGAGAGCTAG CAGCTG CCGACCGCCCTTACCGATTGTTGACCA 326
DB 825 CAACTCTTCAGGCTG CTGAGAGCTAG CAGCTG CCGACCGCCCTTACCGATTGTTGACCA 884
QY 327 GGGCTGGGCGCCCT ATCAGTTATGC CAAACG GAGCGGCCCGACCGAGCGCCCTACTGCTG 386
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QY 387 GCATACCCCGCCAAA AACCCTTGGCG TATTGTG CCGCGGAAGAGTGTGTGTCGCGTATA 446
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DB 1065 CAGCTGGGGTGAAAA TGTATACGAG CGTCTTC GTCCTTAA CAATAC CAGCGCCACCGCTGGG 1124
QY 567 CAAATTGGTTCCGTT GTACTGATGAA CTTAACT GGAATTCAC CAAAGTGTGCGGAGCGCC 626
DB 1125 CAAATTGGTTCCGTT GTACTGATGAA CTTAACT GGAATTCAC CAAAGTGTGCGGAGCGCC 1184
QY 627 TCCTTGTGTGTCATC GCGAGGGCGG GCAACA AACCCCTG CACTGCC CCACTGATTGCTTCCG 686
DB 1185 TCCTTGTGTGTCATC GCGAGGGCGG GCAACA AACCCCTG CACTGCC CCACTGATTGCTTCCG 1244
QY 687 CAAAGCATCCGAGC GCGCACATACT CTCTCG GTGCGGCTCC GGTCCCTGGATCACACCCAGGTG 746
DB 1245 CAAAGCATCCGAGC GCGCACATACT CTCTCG GTGCGGCTCC GGTCCCTGGATCACACCCAGGTG 1304
QY 747 CTTGCTGCACTACCC GGTATAGCTT TGGCAATT ATCTTGT GACCATCA CTAACATATT 806
DB 1305 CTTGCTGCACTACCC GGTATAGCTT TGGCAATT ATCTTGT GACCATCA CTAACATATT 1364
QY 1305 CCTGGTCCGACTAC CCGGTATAGG CTTTGGC ATTATC CTTGTAC CATCAACTACACTATA TT 1364
QY 807 TAAATCAGAGTGTAC GTGGGAGGGTC GAACACA CAGGCTGGA AGCTGCTGCAACTGGAC 866
DB 1365 TAAATCAGAGTGTAC GTGGGAGGGTC GAACACA CAGGCTGGA AGCTGCTGCAACTGGAC 1424
QY 867 GCGGGCGGAAACGTT GCGATCTGGA AGATAGG GACAGGTCC GAGATC 912
DB 1425 GCGGGCGGAAACGTT GCGATCTGGA AGATAGG GACAGGTCC GAGATC 1470

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```

RESULT 6
US-09-742-659-3
; Sequence 3, Application US/09742659
; Patent No. US20010034019A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Zhi
; APPLICANT: Butkiewicz, Nancy J.
; APPLICANT: Zhong, Weidong
; APPLICANT: Ingravallo, Paul
; APPLICANT: Wright-Minogue, Jacquelyn
; APPLICANT: Lau, Johnson Y.
; APPLICANT: Lemon, Stanley M.
; TITLE OF INVENTION: Chimeric HCV/GBV-B viruses
; FILE REFERENCE: ID01116
; CURRENT APPLICATION NUMBER: US/09/742,659

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QY 327 GGGCTGGGCGCTTATCAGTTATGCCAAAGAGCGGCCCGACAGCGCCCTACTGCTG 386  
 Db 1742 GGGCTGGGCTTATCAGTTATGCCAAAGAGCGGCCCTCGAGCAAGCGCCCTACTGCTG 1801  
 QY 387 GCACTACCCCGCCAAAACCTTGGCGGTATTTGCCCGGAAAGAGTGTGTGGTCCGGTATA 446  
 Db 1802 GCACTACCCCTCCAAAGACCTTGTGGCATTTGTGCCCGCAAGAGCGTGTGTGGCCGGTATA 1861  
 QY 447 TTGCTTCACTCCAGCGCCCGTGTGTGGAAAGCAGCAGCAGTGTGGGGCGGCCACCTTA 506  
 Db 1862 TTGCTTCACTCCAGCGCCCGTGTGTGGAAAGCAGCAGCAGTGTGGGGCGGCCCTACCTTA 1921  
 QY 507 CAGCTGGGTGAAATGATACGACGCTTTCGTCTTAACAATPACCAAGCAGCAGCGCTGGG 566  
 Db 1922 CAGCTGGGTGAAATGATACGACGCTTTCGTCTTAACAATPACCAAGCAGCAGCGCTGGG 1981  
 QY 567 CAATTGCTTGGGTGTACCTGATGAACCTCAACTGGATTTCACCAAGTGTGGAGCGCC 626  
 Db 1982 CAATTGCTTGGGTGTACCTGATGAACCTCAACTGGATTTCACCAAGTGTGGAGCGCC 2041  
 QY 627 TCCTTGTGATCGAGGGCGGGCAACAAACCCCTGCACTGCGCCCACTGATTGCTTCCG 686  
 Db 2042 CCCTTGTGATCGAGGGCGGGCAACAAACCCCTTGCCTGCGCCCACTGATTGTTCCG 2101  
 QY 687 CAAGCATCCGAGCGCCACATACCTCGTCCGCTCGGTCGGTCCCTGGATCACACCCAGGTG 746  
 Db 2102 CAAGCATCCGAGCGCCACATACCTCGTCCGCTCGGTCGGTCCCTGGATCACACCCAGGTG 2161  
 QY 747 CTGCTCGACTACCCCGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACACCATATT 806  
 Db 2162 CATGCTCGACTACCCCGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACACCATATT 2221  
 QY 807 TAAATCAGATGTAGTGGAGGGGTGCAACACAGCTGGAAGCTGCCTGCACTGCACTGGAC 866  
 Db 2222 CAAAGTCAGATGTAGTGGAGGGGTGCAACACAGCTGGAAGCTGCCTGCACTGGAAGCTG 2281  
 QY 867 GCGGGCGAAGCTTGCATCTGGAAGTATGGGACAGCTCCGAGATC 912  
 Db 2282 GCGGGCGAAGCTTGCATCTGGAAGTATGGGACAGCTCCGAGCTC 2327

RESULT 8

US-09-995-937-1  
 ; Sequence 1, Application US/09995937  
 ; Publication No. US20030028010A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RICE, CHARLES et al.  
 ; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400  
 ; CITY: ST. LOUIS  
 ; STATE: MO  
 ; COUNTRY: USA  
 ; ZIP: 63105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/995,937  
 ; FILING DATE: 28-No. US20030028010A1-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/034,756  
 ; FILING DATE: 04-May-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: HOLLAND, DONALD R.  
 ; REGISTRATION NUMBER: 35,197  
 ; REFERENCE/DOCKET NUMBER: 6029-4831

TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 314-727-5188  
 ; TELEFAX: 314-727-6092  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9646 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cdna  
 ; HYPOTHEetical: NO  
 ; ANTI-SENSE: NO  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-995-937-1  
 Query Match 46.8%; Score 745.2; DB 10; Length 9646;  
 Best Local Similarity 90.1%; Pred. No. 6.4e-237;  
 Matches 798; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 QY 27 CTGTGTGCTGCTGTGTGGAGCAGTCTTCGTTTCGCCCGCAGCGCTAGCGAAACCCACCT 86  
 Db 1442 CTGGCGGAAGTCTGTGTAGTCTGCTGCTATTTCGCGGCTCGAGCGGAAACCCACCT 1501  
 QY 87 CACCGGGGGAAGTGCCTGGCCCAACACTGTGTCTGGATTGTTAGCTCTCTCGCACCGGCG 146  
 Db 1502 CACCGGGGGAAGTGCCTGGCCCGCACCAAGCTGGCTTGTGGTCTCTTACACCGGCGC 1561  
 QY 147 CAAGCAGAACGTCCAGCTGATCAACACCAACCGGAGTGTGGCACTCAATAGCAGCGCT 206  
 Db 1562 CAAGCAGAACATCCAACTGATCAACCAACCGGAGTGTGGCACTCAATAGCAGCGCT 1621  
 QY 207 GAATGCAATGATAGCTCAACACCGGCTGTGTGGCAGGCTTTTCTATCACCAAGTT 266  
 Db 1622 GAATGCAATGAAAGCCTTAAACCGCTGTTAGCAGGCTCTTCTATCAGACAAAT 1681  
 QY 267 CAACTCTTCAGGCTGTCTGAGAGCTAGCAGCTGCCAGCCCTTACCGATTTTGACCA 326  
 Db 1682 CAACTCTTCAGGCTGTCTGAGAGTGTGGCCAGCTGCCAGCCTTACCGATTTTGCCCA 1741  
 QY 327 GGGCTGGGCGCTATCAGTTATGCCAAGAGCGGCCCGGACCGCCCTACTGCTG 386  
 Db 1742 GGGCTGGGCTCTATCAGTTATGCCAAGAGCGGCTTCGACAAACCGCCCTACTGCTG 1801  
 QY 387 GCACTACCCCGCCAAAACCTTGGGTATTTGTCGCCGGAAGAGTGTGTGTGTCGGTATA 446  
 Db 1802 GCACTACCTCCAAAGACCTTGTGGCATTTGTGCCCGCAAGAGCGTGTGTGGCCGGTATA 1861  
 QY 447 TTGCTTCACTCCAGCGCCCGTGTGTGGAAAGCAGCAGCTCGGCGCGGCCACCTTA 506  
 Db 1862 TTGCTTCACTCCAGCGCCCGTGTGTGGAAAGCAGCAGCTCGGCGCGGCCCTACCTTA 1921  
 QY 507 CAGCTGGGTGAAATGATACGACGCTTTCGTCTTAACAATPACCAAGTGTGGAGCGCC 566  
 Db 1922 CAGCTGGGTGAAATGATACGACGCTTTCGTCTTAACAATPACCAAGTGTGGAGCGCC 1981  
 QY 567 CAATTGCTTGGGTGTACCTGATGAACCTCAACTGGATTTCACCAAGTGTGGAGCGCC 626  
 Db 1982 CAATTGCTTGGGTGTACCTGATGAACCTCAACTGGATTTCACCAAGTGTGGAGCGCC 2041  
 QY 627 TCCTTGTGATCGAGGGCGGGCAACAAACCCCTGCACTGCGCCCACTGATTGCTTCCG 686  
 Db 2042 CCCTTGTGATCGAGGGGTGGGCAACAAACCCCTTGCCTGCGCCCACTGATTGTTCCG 2101  
 QY 687 CAAGCATCCGAGCGCCACATACCTCGTCCGCTCGGTCGGTCCCTGGATCACACCCAGGTG 746  
 Db 2102 CAAGCATCCGAGCGCCACATACCTCGTCCGCTCGGTCGGTCCCTGGATCACACCCAGGTG 2161  
 QY 747 CTGCTCGACTACCCCGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACACCATATT 806  
 Db 2162 CATGCTCGACTACCCCGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACACCATATT 2221  
 QY 807 TAAATCAGATGTAGTGGAGGGGTGCAACACAGCTGGAAGCTGCCTGCACTGGAAGCTG 866

Db 2222 CAAAGTCAGGATGATCGTGGAGGGTTCGAGCAGCAGGCTGGAGCGCCTGCAACTGGAC 2281  
 QY 867 GCGGGCGGAACGTTGCGATCTGGAAGATAGGAGCAGGTCGAGATC 912  
 Db 2282 GCGGGCGGAACGTTGATCTGGAAGACAGGACAGGTCGAGCTC 2327

RESULT 9

US-09-917-563-1  
 ; Sequence 1, Application US/09917563  
 ; Publication No. US20030073080A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RICE, CHARLES et al.  
 ; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C  
 ; VIRUS (HCV) AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400  
 ; CITY: ST. LOUIS  
 ; STATE: MO  
 ; COUNTRY: USA  
 ; ZIP: 63105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA: US/09/917,563  
 ; FILING DATE: 27-Jul-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/238,076  
 ; FILING DATE: 26-JAN-1999  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: HOLLAND, DONALD R.  
 ; REGISTRATION NUMBER: 35,197  
 ; REFERENCE/DOCKET NUMBER: 6029-4831  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 314-727-5188  
 ; TELEFAX: 314-727-6092  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 9646 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-917-563-1  
 Query Match 46.8%; Score 745.2; DB 10; Length 9646;  
 Best Local Similarity 90.1%; Pred. No. 6.4e-237;  
 Matches 798; Conservative 0; Mismatches 88; Indels 0; Gaps 0;  
 QY 27 CTGTGCTGCTGCTGTGGAGCAGTCTTCGTCGCCAGCGCTAGCGAACCACGT 86  
 Db 1442 CTGGGCGAAGTCTTGTTAGTCTGCTATTTGCCGCGCTCGACGGGAAACCCAGT 1501  
 QY 87 CACCGGGGAAGTGGCGGCACACTGTGTCGATTGTAGCCTCTCGACACGAGGCGC 146  
 Db 1502 CACCGGGGAAGTGGCGGCACACCGCTTGTGTCTCTTACACGAGGCGC 1561  
 QY 147 CAAGCAGAACGTCCAGCTGATCAACACCGCAGTGTGGCAGCTCAATAGCAGCGCCT 206  
 Db 1562 CAAGCAGAACATCCAACTGATCAACACCGCAGTGTGGCAGCTCAATAGCAGCGCTT 1621  
 QY 207 GAACTGCAATGATAGCTCAACACCGGCTGGTGGCAGGGCTTTTCTATCACCACAGTT 266  
 Db 1622 GAACTGCAATGAAGCCTTAAACCGGCTGGTGGCAGGGCTTCTTATCAGCACAAATT 1681

QY 267 CAACTCTTCAGGCTGCTCCTGAGAGGCTAGCCAGCTCCGACCCCTTTACCGATTTTTCACCA 356  
 Db 1682 CAACTCTTCAGGCTGCTCCTGAGAGGTTGGCCAGCTGCCGACGGCTTACCGATTTTTCACCA 1741  
 QY 327 GGGCTGGGGCCCTATCAGTTATGCGAAGCGGCGCCGACAGCGGCGGCTTACTGCTG 386  
 Db 1742 GGGCTGGGGTCTCTATCAGTTATGCGAAGCGGCGCTCGACGACGCGGCTTACTGCTG 1801  
 QY 387 GCACCTACCCCGCAAAACCTTGGGTTATGTCGCCCGGAGAGAGTGTGTGGTCCGGTATA 446  
 Db 1802 GCACCTACCCCTCCAAAGACCTTGTGGCATTGTGCCCGCAAGAGCGGTGTGTGGCCGGTATA 1861  
 QY 447 TTGCTTCACTCCAGCGCCCGTGGTGGGAAACGACCGACAGGTTCGGGCGCGCCACCTA 506  
 Db 1862 TTGCTTCACTCCAGCGCCCGTGGTGGGAAACGACCGACAGGTTCGGGCGCGCTTACTA 1921  
 QY 507 CAGCTGGGGTGAANAATGATACGAGCGTCTTCTCTTAAACAATACAGCGACCGCTGGG 566  
 Db 1922 CAGCTGGGGTGAANAATGATACGAGCGTCTTCTCTTAAACAATACAGCGACCGCTGGG 1981  
 QY 567 CAATTGGTTTCGGTTCTGCTGATGAACTCAACTGGATTTCACCAAGTGTGGGAGCGCC 626  
 Db 1982 CAATTGGTTTCGGTTCTGCTGATGAACTCAACTGGATTTCACCAAGTGTGGGAGCGCC 2041  
 QY 627 TCCTTGTGTCTCAGGAGGGCGGCAACAAACCCCTGCACTGCCCTGCTGCTTTCCTG 686  
 Db 2042 CCCTTGTGTCTCAGGAGGGTGGGCAACAAACCTTGTCTGCCCTGCTGCTTTCCTG 2101  
 QY 687 CAAGCATCCGAGCGCCACATCTCTCGGTGGGCTCCGCTCCGATCAGCAGGCTG 746  
 Db 2102 CAAGCATCCGAGCGCCACATCTCTCGGTGGGCTCCGCTCCGATCAGCAGGCTG 2161  
 QY 747 CCGTGGTCTGCTGCTGATAGGCTTGGCATTTATCTTGTACCATCACTACCATATT 806  
 Db 2162 CATGCTGCTGCTGCTGATAGGCTTGGCATTTATCTTGTACCATCACTACCATATT 2221  
 QY 807 TAAATCAGGATGATGCTGGAGGGGCTCGAACAAGGCTGGAAGCTGCTGCACTGGAC 866  
 Db 2222 CAACTCAGGATGATGCTGGAGGGGCTCGAACAAGGCTGGAAGCTGCTGCACTGGAC 2281  
 QY 867 GCGGGCGAAGCTTCGATCTGGAAGATAGGAGCAGGTCGAGATC 912  
 Db 2282 GCGGGCGAAGCTTCGATCTGGAAGATAGGAGCAGGTCGAGATC 2327

RESULT 10

US-09-238-076-5  
 ; Sequence 5, Application US/09238076  
 ; Patent No. US20020102540A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RICE, CHARLES et al.  
 ; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C  
 ; VIRUS (HCV) AND USES THEREOF  
 ; NUMBER OF SEQUENCES: 21  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
 ; STREET: 7733 FORSYTH BLVD., SUITE 1400  
 ; CITY: ST. LOUIS  
 ; STATE: MO  
 ; COUNTRY: USA  
 ; ZIP: 63105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/238,076  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 09/034,756

/	FILING DATE:							
/	ATTORNEY/AGENT INFORMATION:							
/	NAME: HOLLAND, DONALD R.							
/	REGISTRATION NUMBER: 35,197							
/	REFERENCE/DOCKET NUMBER: 6029-4831							
/	TELECOMMUNICATION INFORMATION:							
/	TELEPHONE: 314-727-5188							
/	TELEFAX: 314-727-6092							
/	INFORMATION FOR SEQ ID NO: 5:							
/	SEQUENCE CHARACTERISTICS:							
/	LENGTH: 12980 base pairs							
/	TYPE: nucleic acid							
/	STRANDEDNESS: double							
/	TOPOLOGY: linear							
/	MOLECULE TYPE: cDNA							
/	HYPOTHETICAL: NO							
/	ANTI-SENSE: NO							
/	US-09-238-076-5							
Qy	Query Match	46.8%;	Score	745.2;	DB 9;	Length	12980;	
Db	Best Local Similarity	90.1%;	Pred. No.	7.5e-237;	Mismatches	0;	Gaps	0;
Qy	Matches	798;	Conservative	0;	Indels	88;		
Qy	27	CTGTGTCCTGCTGTGTGGAGAGTCTTCGTTTGCCCGCAGCGTAGAGAAACCCACGT	86					
Db	1442	CTGGCGAAGGTCTCTGTAGTGTCTGTCTATTTGCCGGCGTCGACGCGGAACCCACGT	1501					
Qy	87	CACCGGGGAAGTCGCGGCACACTGTGCTGGATTGTTAGCTCTCTGCACCAGGCGC	146					
Db	1502	CACCGGGGAAGTCGCGGCACCAACCGCTGGGCTTGTGGTCTCTTACACAGGCGC	1561					
Qy	147	CAAGCAGAACGCTCCAGCTGATCAACCAACGGCAGTTGGCACCTCAATAGCACGGCCCT	206					
Db	1562	CAAGCAGAACATCCAATCATCAACCAACGGCAGTTGGCACATCAATAGCACGGCCCT	1621					
Qy	207	GAACCTGAATGATAGCTCAACACCGCTGGTTGGCAGGGCTTTCTATCACCACAAGTT	266					
Db	1622	GAACCTGAATGAAGCCCTTAACACCGCTGGTTAGCAGGGCTCTTCTATCAGCACAAAT	1681					
Qy	267	CAACTCTTCAGGCTGTCTGAGAGCTAGCCAGCTGCCGACCCCTTACCAGATTTGACCA	326					
Db	1682	CAACTCTTCAGGCTGTCTGAGAGTTGGCCAGCTGCCAGCGCTTACCGATTTGCCCCA	1741					
Qy	327	GGGCTGGGGCCCTATCAGTTATGCCAACGGAGCGGCCGACGAGCGCCCCTACTGCTG	386					
Db	1742	GGGCTGGGGTCCTATCAGTTATGCCAACGGAGCGGGCTCGACGAACGCCCTACTGCTG	1801					
Qy	387	GCATCTACCCCAAACCTTCGCGTATTGTGCCCGCAAGAGTGTGTGGTCCGGTATA	446					
Db	1802	GCATCTACCCCTCAAAGACTTGTGGCATTGTGCCCGCAAGAAGCGTGTGTGGCCGGTATA	1861					
Qy	447	TTCCTTCACTCCAGCCCGTGTGGTGGGAACGACGACGAGTCGGCGCGGCCACCTA	506					
Db	1862	TTCCTTCACTCCAGCCCGTGTGGTGGGAACGACGACGAGTCGGCGCGGCCCTACTTA	1921					
Qy	507	CAGCTGGGTGAAAATGATACGACGCTTCGTCCTTAACAATACCAAGGCCACCGCTGGG	566					
Db	1922	CAGCTGGGTGCAAATGATACGAGTGTCTCGTCTTAAACAACCAACCAAGGCCACCGCTGGG	1981					
Qy	567	CAATTGGTTTCGGTTGTACTCGATGAATCAACTCGGATTCAACCAAGTGTGCGGAGGCC	626					
Db	1982	CAATTGGTTTCGGTTGTACTCGATGAATCAACTCGGATTCAACCAAGTGTGCGGAGGCC	2041					
Qy	627	TCTTGTGTATCGAGGGGGCGGCAACAACCCCTGCACTGCCCCCACTGATTCCTCCG	686					
Db	2042	CCCTTGTGTATCGAGGGGTGGGCAACAACACCTTGTCTGCCCCCACTGATTTTTCGG	2101					
Qy	687	CAAGCATCCGACGCCACATACTCTCGTGGGGTCCGGTCCCTGGGATCACACCCAGGTG	746					
Db	2102	CAAGCATCCGAAGGCCAATACTCTCGTGGGGTCCGGTCCCTGGGATTAACCCAGGTG	2161					
Qy	747	CCTGTCGACTACCGGTATAGGCTTTGGCATTTATCTTGTACCATCAACTACCATATT	806					

Db	2162	CATGGTCGACTACCCGTTAGGCTTTGGCACTATCCTTGTACCATCAATTACACCATATT	2221
Qy	807	TAAATACAGGATGTACGTGGGAGGGTTCGAACACAGGCTGGGAAGCTGCCTGCAACTGGAC	866
Db	2222	CAAAGTCAGGATGTACGTGGGAGGGTTCGAGCACAGGCTGGGAAGGGCCCTGCAACTGGAC	2281
Qy	867	GCGGGGCGGAACGTTGCGATCTCGAAGATAGGCACAGGTCGAGATC	912
Db	2282	GCGGGGCGGAACGCTGTGTCTGTGAAGACAGGGACAGGTCGAGCTC	2327
RESULT 11			
US-09-995-937-5			
; Sequence 5, Application US/09995937			
; Publication No. US20030028010A1			
; GENERAL INFORMATION:			
; APPLICANT: RICE, CHARLES et al.			
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C			
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF			
; NUMBER OF SEQUENCES: 21			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.			
; STREET: 7733 FORSYTH BLVD., SUITE 1400			
; CITY: ST. LOUIS			
; STATE: MO			
; COUNTRY: USA			
; ZIP: 63105			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent in Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/09/995,937			
; FILING DATE: 28-No. US20030028010A1-2001			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/09/034,756			
; FILING DATE: 04-May-1998			
; ATTORNEY/AGENT INFORMATION:			
; NAME: HOLLAND, DONALD R.			
; REGISTRATION NUMBER: 35,197			
; REFERENCE/DOCKET NUMBER: 6029-4831			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: 314-727-5188			
; TELEFAX: 314-727-6092			
; INFORMATION FOR SEQ ID NO: 5:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 12980 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: double			
; TOPOLOGY: linear			
; MOLECULE TYPE: cDNA			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:			
US-09-995-937-5			

	Query Match	46.8%	Score 745.2;	DB 10;	Length 12980;
	Best Local Similarity	90.1%;	Pred. No. 7.5e-237;		
	Matches 799;	Conservative 0;	Mismatches 88;	Indels 0;	Gaps 0;
Qy	27	CTGTGTCTCTCTCTGTGTGAGCAGTCTCTGTTTGCSCCAGCGCTAGCGAAACCCACGT	86		
Db	1442	CTGGCGGAAGTCTCTGTAGTGTCTGTCTATTGTTCGGGCGTGCAGCGGNAACCCACGT	1501		
Qy	87	CACCGGGGAAGTGC CGGCGCACACTGTGTCGTGATTTGTTTAGCTCTCTCGCACGAGCGC	146		
Db	1502	CACCGGGGAAGTGC CGGCGCGCACACCGGCTGGGCTTGTGTCTCTTACACCGAGCGC	1561		
Qy	147	CAGCAGAACGTCACGTGATCAACACCAACGCGAGTTGGCCTCAATAGCAGCGCCCT	206		
Db	1562	CAGCAGAACATCCAATGATCAACACCAACGCGAGTTGGCACAATATGACAGCGCCTT	1621		



207 GAACTGCAATGATAGCCTCAACACCGGCTGGTTGGCAGGCTTTTCTATCACCAAGTT 266  
1622 GAACTGCAATGAAAGCCTTAACACCGGCTGGTTAGCAGGCTCTTCTATCAGCAAAAT 1681  
267 CAATCTTTAGGCTGCTGAGAGGTAGCAGCTGCGACCCCTTACCGATTTTGACCA 326  
1682 CAATCTTTAGGCTGCTGAGAGGTGGCCAGCTGCGACGCTTACCGATTTTGCCCA 1741  
327 GGGCTGGGCGCTTACAGTTATGCCAAGGAGCGGCCCGACGAGCGCCCTACTGCTG 386  
1742 GGGCTGGGCTTATCAGTTATGCCAAGGAGCGGCCCTGAGAAAGCGCCCTACTGCTG 1801  
387 GCATACCCCGGCTTGGCTGTTGTCGCGGAGAGGTGTTGTTGGTCCGCTATA 446  
1802 GCATACCCCTCAAGACCTTGTGCGATTTGTCGCGCAAGAGCGTGTGTGGCCGCTATA 1861  
447 TTGCTTCACTCCAGCGCGCTGTTGTTGGGAACGACGACGAGTGGCGGCGCCACCTA 506  
1862 TTGCTTCACTCCAGCGCGCTGTTGTTGGGAACGACGACGAGTGGCGGCGCTACCTA 1921  
507 CAGCTGGGTGAAATGATACGACGCTTTTCGTCCTTAAACAATACCAGGCGCCGCTGG 566  
1922 CAGCTGGGTGCAATGATACGAGTGTCTTCTGCTTTAAACAACACGAGCGCCGCTGG 1981  
567 CAATTCGTTGCTGTTGACCTGGATGAATCAACTGGATTTACCAAAAGTGTGGCGAGCG 626  
1982 CAATTCGTTGCTGTTGACCTGGATGAATCAACTGGATTTACCAAAAGTGTGGCGAGCG 2041  
627 TCCTTGTGTCATCGGAGGGCGGCAACACACCTTGACCTGCGCCCACTGATTTGCTCG 686  
2042 CCCTTGTGTCATCGGAGGGGTGGGCAACACACCTTGTCTGCCCCACTGATTTGCTCG 2101  
687 CAAGCATCCGAGCGCCACATACCTCTCGGTGGGCTCCGCTCCGCTGATCACCCAGGTG 746  
2102 CAAGCATCCGAGCGCCACATACCTCTCGGTGGGCTCCGCTCCGCTGATCACCCAGGTG 2161  
747 CTGCTGCGACTACCCGCTATAGGCTTTGGCATTTATCTTGTACCATCAACTACACCATAT 806  
2162 CATGTCGACTACCCGCTATAGGCTTTGGCACTATCTTGTACCATCAATTACACCATAT 2221  
807 TAAATCAGATGATAGCTGGAGGGGTGAAACACAGCTGGAGCTGCACTGCACTGAC 866  
2222 CAAAGTCAGATGATAGCTGGAGGGGTGAGACACAGCTGGAAGCGGCTGCAACTGGAC 2281  
867 GCGGGCGAAGCTTGGATCTCGAATAGGAGCAGGTCGAGATC 912  
2282 GCGGGCGAAGCTGATGATCTGGAAGACAGGACAGGTCGAGCTC 2327

RESULT 12

US-09-917-563-5  
; Sequence 5, Application US/09917563  
; Publication No. US20030073080A1  
; GENERAL INFORMATION:  
; APPLICANT: RICE, CHARLES et al.  
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C  
; VIRUS (HCV) AND USES THEREOF  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BLVD., SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/917,563

; FILING DATE: 27-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/238,076  
; FILING DATE: 26-JAN-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 6029-4831  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12980 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-917-563-5

Query Match 46.8%; Score 745.2; DB 10; Length 12980;

Best Local Similarity 90.1%; Pred. No. 7.5e-237;

Matches 798; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 27 CTGTGTGCTGCTGTGTGGAGAGTCTTCTGTCGCGGCGGCTGAGGAAACCCACGT 86  
Db 1442 CTGGCGAAGTCTGTGTGCTATTTGCGCGCTCGACGCGAAACCCACGT 1501  
QY 87 CACCGGGGAAGTGGCGGCACACTGTGTCGATTTGTTAGCTCTCGCACCGGCGC 146  
Db 1502 CACCGGGGAAGTGGCGGCGGCACGCTGTTGTTGCTCTTACACGAGCGC 1561  
QY 147 CAAGCAGAACGTCAGCTGATCAACACCAACGCGAGTTGGCACCTCAATAGCACGCGCT 206  
Db 1562 CAAGCAGAACATCCAACTGATCAACACCAACGCGAGTTGGCACATCAATAGCACGCGCT 1621  
QY 207 GAACTGCAATGATAGCTCAACACCGGCTGTTGGAGGCTTTTCTATCACCAAGTT 266  
Db 1622 GAACTGCAATGAAAGCTTAAACCGGCTGTTAGCAGGCTCTTCTATCAGCACAAAT 1681  
QY 267 CAACTCTTCAGGCTGCTGAGAGCTAGCAGCTGCGACCCCTTACCGATTTTGACCA 326  
Db 1682 CAACTCTTCAGGCTGCTGAGAGGTGGCGAGCTGGCGACGCTTACCGATTTTGCCCA 1741  
QY 327 GGGCTGGGCGCTTATCAGTTATGCCAAGGAGCGGCCCGACGAGCGCCCTACTGCTG 386  
Db 1742 GGGCTGGGCTCTATCAGTTATGCCAAGGAGCGGCTCGACGAAAGCGCCCTACTGCTG 1801  
QY 387 GCATACCCCGCAAAACCTTGGGCTATTTGTCGCGGAGAGTGTGTGTGTCGCTATA 446  
Db 1802 GCATACCCCTCCAGACCTTGTGGCATTTGTGCGCGCAAGAGCGTGTGTGGCCGCTATA 1861  
QY 447 TTGCTTCACTCCAGCGCGCTGTTGGGAACGACGACGAGTGGCGGCGCCACCTA 506  
Db 1862 TTGCTTCACTCCAGCGCGCTGTTGGGAACGACGACGAGTGGCGGCGCTTACCTA 1921  
QY 507 CAGCTGGGCTGAAATGATAGCAGCTCTTCTGCTTAAACAATACCAGGCGCCGCTGG 566  
Db 1922 CAGCTGGGCTGCAATGATAGCAGTGTCTTCTGCTTAAACAACACGAGCGCCGCTGG 1981  
QY 567 CAATTCGTTGCTGTTGATCGAATCAACTGAGATTTACCAAAAGTGTGGCGAGCGC 626  
Db 1982 CAATTCGTTGCTGTTGATCGAATCAACTGAGATTTACCAAAAGTGTGGCGAGCGC 2041  
QY 627 TCCTTGTGTCATCGGAGGGCGGCAACACACCTTGACCTGCGCCCACTGATTTGCTCG 686  
Db 2042 CCCTTGTGTCATCGGAGGGGTGGGCAACACACCTTGTCTGCCCCACTGATTTGCTCG 2101  
QY 687 CAAGCATCCGAGCGCCACATACCTCTCGGTGGGCTCCGCTCCGCTGATCACACCGAGGTG 746





Search completed: April 15, 2005, 04:52:24  
Job time : 1000 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: April 14, 2005, 21:43:49 ; Search time 5460 Seconds  
(without alignments)  
11105.564 Million cell updates/sec

Title: US-10-715-665-6\_COPY\_1992\_3584  
Perfect score: 1593  
Sequence: 1 atggatgcaatgaagagagg.....tttgtctctgggtatacatt 1593

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_btc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	4.3	290	5 BQ678991	AGENCOURT
2	69	4.3	300	1 AU100324	AU100324
3	69	4.3	378	1 AA317921	AA317921
4	69	4.3	393	6 CB139652	K-EST0192
5	69	4.3	469	7 CN268878	170004247
6	69	4.3	495	2 AW239072	xb36b11.y
7	69	4.3	500	6 CB129127	K-EST0178
8	69	4.3	511	2 BE389162	hw03h06.y
9	69	4.3	531	6 CD672904	fg17f07.y
10	69	4.3	571	1 AU134450	AU134450
11	69	4.3	578	5 BP366704	BP366704
12	69	4.3	580	1 AU138842	AU138842
13	69	4.3	581	7 CN481173	CN481173
14	69	4.3	584	5 BP259505	BP259505
15	69	4.3	593	6 CB131100	CB131100
16	69	4.3	594	7 CN483734	hw36f09.y
17	69	4.3	612	2 BE386111	BE386111
18	69	4.3	616	7 CN268875	170005325
19	69	4.3	620	7 CF132460	UI-HF-FQ0
20	69	4.3	624	2 BE390617	601284976
21	69	4.3	632	1 AU124041	AU124041
22	69	4.3	636	7 CF125573	UI-HF-EL0
23	69	4.3	637	1 AU134370	AU134370
24	69	4.3	641	7 CV027090	5255 Full

25	69	4.3	646	1 AU134236	AU134236
26	69	4.3	646	4 BG477928	602522906
27	69	4.3	650	7 CN268879	170005319
28	69	4.3	658	2 BE384999	601276871
29	69	4.3	680	7 CF264856	AGENCOURT
30	69	4.3	680	7 CN268877	170006001
31	69	4.3	686	7 CF125651	UI-HF-EL0
32	69	4.3	688	7 CO245698	AGENCOURT
33	69	4.3	694	1 AU134787	AL524377
34	69	4.3	694	1 AU134787	AL524377
35	69	4.3	703	2 BE390092	601285720
36	69	4.3	706	1 AU036128	DKF2p5648
37	69	4.3	710	2 BE261317	601148758
38	69	4.3	711	4 BG476511	602522049
39	69	4.3	711	4 BG763226	602735258
40	69	4.3	716	2 BE408331	601302704
41	69	4.3	720	2 BF689648	602187048
42	69	4.3	723	7 CO245365	AGENCOURT
43	69	4.3	740	4 BG768016	602743779
44	69	4.3	755	4 BG761429	602718630
45	69	4.3	761	4 BI771956	603058981

ALIGNMENTS

RESULT 1  
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LOCUS BQ678991 290 bp mRNA linear EST 15-JUL-2002  
DEFINITION AGENCOURT\_8281562 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6262005  
5', mRNA sequence.  
ACCESSION BQ678991  
VERSION BQ678991.1 GI:21791670  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 290)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-rc@mail.nih.gov  
Tissue Procurement: DCTD/DTF  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLCM2423 row: j column: 22  
High quality sequence stop: 289.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

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/organism="Homo sapiens"  
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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 4.3%; Score 69; DB 5; Length 290;



**SOURCE**  
Homo sapiens (human)  
**ORGANISM**  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
1 (bases 1 to 393)  
**AUTHORS**  
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.

**TITLE**  
21C Frontier Korean EST Project 2001  
**JOURNAL**  
Unpublished (2002)  
**COMMENT**  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Soeun-dong yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 19 row: B column: 03  
High quality sequence stop: 393.

**FEATURES**  
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Location/Qualifiers  
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/lab\_host="Top10F"  
/clone\_lib="L15CKK1"  
/note="Organ: Liver; Vector: pCNS-D2; Site\_1: EcoRI;  
Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tabacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including  
EcoRI site by treatment of T4 RNA ligase and the first  
strand cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed vector was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Berg method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library."

**ORIGIN**  
Query Match 4.3%; Score 69; DB 6; Length 393;  
Best Local Similarity 100.0%; Pred.No. 4e-09;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGCTGTGCTGTGAGCAGTCCTCGTT 60  
|||||  
**Db** 101 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGCTGTGCTGTGAGCAGTCCTCGTT 160  
|||||

**QY** 61 TCGCCACG 69  
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**Db** 161 TCGCCACG 169  
|||||

**RESULT 5**  
**CN268878**  
**LOCUS** 17000424723882 GRN\_ES Homo sapiens cDNA 5', mRNA linear EST 16-MAY-2004  
**DEFINITION** CN268878  
**ACCESSION** CN268878.1 GI:47285292  
**VERSION** EST.  
**KEYWORDS** Homo sapiens (human)  
**SOURCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
**ORGANISM** Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 469)  
**AUTHORS** Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,

**SOURCE**  
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,  
Lebkowski,J and Stanton,L.W.  
Transcriptome characterization elucidates signaling networks that  
control human ES cell growth and differentiation  
Nat. Biotechnol. 22 (6) 707-716 (2004)  
Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@geron.com  
Insert Length: 469 Std Error: 0.00.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, cell lines H1, H7, and  
H9"  
/clone\_lib="GRN ES"  
/note="Oligo dt primed, full-length enriched cDNA library  
from undifferentiated hES cell lines H1 (p32), H7 (p29),  
and H9 (p26) maintained in feeder-free conditions"

**ORIGIN**  
Query Match 4.3%; Score 69; DB 7; Length 469;  
Best Local Similarity 100.0%; Pred.No. 4.2e-09;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 1 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGCTGTGCTGTGAGCAGTCCTCGTT 60  
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**Db** 86 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGCTGTGCTGTGAGCAGTCCTCGTT 145  
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**QY** 61 TCGCCACG 69  
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**Db** 146 TCGCCACG 154  
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**RESULT 6**  
**AW239072**  
**LOCUS** xb36b11.y1 NCI CGAP LuJ31 Homo sapiens cDNA clone IMAGE:2578365 5'  
similar to gp:M15518 TISSUE PLASMINOGEN ACTIVATOR PRECURSOR  
(HUMAN); , mRNA sequence.  
**ACCESSION** AW239072  
**VERSION** AW239072.1 GI:6571462  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 495)  
**AUTHORS** NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@email.nih.gov  
Tissue Procurement: ATCC CDNA Library Preparation: Life  
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Seq primer: -40RP from Gibco  
High quality sequence stop: 456.

**FEATURES**  
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Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally, no
5' adaptor. Primer: Oligo dt. Full-length library
constructed by Life Technologies."
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# ORIGIN

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Query Match 4.3%; Score 69; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGAGCAGTCTTCGTT 60
Db 65 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGAGCAGTCTTCGTT 124

QY 61 TCGCCGAGC 69
Db 125 TCGCCGAGC 133
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# RESULT 7

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LOCUS K-EST0178736 L15CKK1 Homo sapiens cDNA clone L15CKK1-4-B07 5', mRNA
DEFINITION
sequence.
ACCESSION CB129127
VERSION CB129127.1 GI:28092559
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 500)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
```

```
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
```

```
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: B column: 07
High quality sequence stop: 500.
Location/Qualifiers
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/lab_host="Top10F"
/clone_lib="L15CKK1"
/notes="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with cabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
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# FEATURES

source

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/organism="Homo sapiens"

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Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with cabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The

# ORIGIN

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Query Match 4.3%; Score 69; DB 6; Length 500;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
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QY 1 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGAGCAGTCTTCGTT 60
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QY 61 TCGCCGAGC 69
Db 296 TCGCCGAGC 304
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# RESULT 8

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LOCUS 601285961F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607767 5',
DEFINITION mRNA sequence.
ACCESSION BE389162
VERSION BE389162.1 GI:9334527
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 511)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM259 row: i column: 16
High quality sequence stop: 510.
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/notes="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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# FEATURES

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3607767"

/tissue\_type="endometrium, adenocarcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 44"

/notes="Organ: uterus; Vector: pOTB7; Site\_1: XhoI; Site\_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

# ORIGIN

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Query Match 4.3%; Score 69; DB 2; Length 511;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGAGCAGTCTTCGTT 60
Db 58 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGTGTGAGCAGTCTTCGTT 117

QY 61 TCGCCGAGC 69
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Db	118 TCGCCGAGC 126 
RESULT 9	
CD672904	531 bp mRNA linear EST 24-JUN-2003
LOCUS	f91f07.y1 Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone
DEFINITION	f91f07 5', mRNA sequence.
ACCESSION	CD672904
VERSION	EST.
KEYWORDS	Homo sapiens
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 531) Wistow G., Bernstein S.L., Rav S., Wyatt M.K., Behal A., Touchman J.W., Bouffard G., Smith D. and Peterson K., Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium Mol. Vis. 8 (4), 185-195 (2002)
AUTHORS	Mol. Vis. 8 (4), 185-195 (2002)
TITLE	Contact: Wistow G
JOURNAL	Section on Molecular Structure and Function
MEDLINE	National Eye Institute
PUBMED	6/331, NIH, Bethesda, MD 20892-2740, USA
COMMENT	Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 17 row: f column: 07 Seq primer: M13Rpl reverse primer (ABT). Location/Qualifiers 1..531 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="fg17f07" /tissue_type="iris" /dev_stage="Adult" /lab_host="EMDH10B" /clone_lib="Human Iris cDNA (Normalized): fg" /note="Organ: Eye; Vector: pCMVSPORT6; A human iris library (bx) was normalized by self-subtraction. One portion of double stranded plasmid DNA representing the library was linearized by NotI. This NotI digested library was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."
FEATURES	source
ORIGIN	
Query Match	4.3%; Score 69; DB 6; Length 531;
Best Local Similarity	100.0%; Pred. No. 4.3e-09;
Matches	69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGGATGCATGAAGAGAGGGCTTCGTGTGCTGCTGTGTTGGAGCAGCTTCGTT 60 
Db	113 ATGGATGCATGAAGAGAGGGCTTCGTGTGCTGCTGTGTTGGAGCAGCTTCGTT 172 
Qy	61 TCGCCGAGC 69 
Db	173 TCGCCGAGC 181 
RESULT 10	
AUI134450	571 bp mRNA linear EST 01-AUG-2003
LOCUS	AUI134450 OVARC1 Homo sapiens cDNA clone OVARC1001993 5', mRNA
DEFINITION	sequence.
ACCESSION	AUI134450
VERSION	GI:10994989
KEYWORDS	EST.
SOURCE	Homo sapiens
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 571) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yanamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T. HRI human cDNA project Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1..571 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="OVARC1001993" /tissue_type="ovary, tumor tissue" /clone_lib="OVARC1" /note="Vector: pME18SFL3"
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	source
ORIGIN	
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Best Local Similarity	100.0%; Pred. No. 4.4e-09;
Matches	69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGGATGCATGAAGAGAGGGCTTCGTGTGCTGCTGTGTTGGAGCAGCTTCGTT 60 
Db	99 ATGGATGCATGAAGAGAGGGCTTCGTGTGCTGCTGTGTTGGAGCAGCTTCGTT 158 
Qy	61 TCGCCGAGC 69 
Db	159 TCGCCGAGC 167 
RESULT 11	
BP366704	578 bp mRNA linear EST 17-SEP-2004
LOCUS	BP366704 Sugano cDNA library, thymus Homo sapiens cDNA clone
DEFINITION	TMS011388, mRNA sequence.
ACCESSION	BP366704
VERSION	EST.
KEYWORDS	Homo sapiens
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 578) Mizushima-Sugano,J., Nakai,K. and Sugano,S. Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004) Contact: Yutaka Suzuki Department of Virology
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	source
ORIGIN	
Query Match	4.3%; Score 69; DB 6; Length 531;
Best Local Similarity	100.0%; Pred. No. 4.3e-09;
Matches	69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGGATGCATGAAGAGAGGGCTTCGTGTGCTGCTGTGTTGGAGCAGCTTCGTT 60 
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Qy	61 TCGCCGAGC 69 
Db	173 TCGCCGAGC 181 

[illegible]



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DEFINITION BP259505 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT07003, mRNA sequence.
ACCESSION BP259505
VERSION BP259505.1 GI:52174735
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 584)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..584
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRT07003"
/tissue_type="heart"
/clone_lib="Sugano cDNA library, heart"

ORIGIN
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Best Local Similarity 100.0%; Pred.No. 4.5e-09;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 99 ATGGATGCAATGAAGAGAGGGCTCTGCTGTGCTGCTGTGCTGTGCTGTGCTGTTCGTT 158

QY 61 TCGCCCCAGC 69
DB 159 TCGCCCCAGC 167

RESULT 15
LOCUS CB131100
DEFINITION K-EST0181101 L12JSHCO Homo sapiens cDNA clone L12JSHCO-11-A02 5',
mRNA sequence.
ACCESSION CB131100
VERSION CB131100.1 GI:28095614
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 593)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yusong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 11 row: A column: 02
High quality sequence stop: 593.
Location/Qualifiers
1..593
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